

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(ii) TITLE OF INVENTION: Methods of Ex-vivo Expansion of Hematopoietic Cells Using Interleukin-3 (IL-3) Multiple Mutation Polypeptides

(iii) NUMBER OF SEQUENCES: 415

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
(B) FILING DATE: 04-MAR-2002
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/764,114
(B) FILING DATE: 09-DEC-1996

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/981,044
(B) FILING DATE: 24-NOV-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US93/11197
(B) FILING DATE: 22-NOV-1993

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/411,795
(B) FILING DATE: 04-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

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(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTAGCGATCT TTTAATAAGC TTG

23

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCCAAGCT TATTAAAGA TCG

23

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCAACAATT TCTACAAAAC ACTTGATACT GTATGAGCAT ACAGTATAAT TGCTTCAACA

60

GAACAGATC

69

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGTTCTGTTG AAGCAATTAT ACTGTATGCT CATACAGTAT CAAGTGTTTT GTAGAAATTG 60

TTGCCGC 67

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCATTGCTGC CGGCATCGTG GTC 23

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CATGGCTCCA ATGACTCAGA CTACTTCTCT TAAGACTTCT TGGGTT 46

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACCCAAGAA GTCTTAAGAG AAGTAGTCTG AGTCATTGGA GC 42

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AATTCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT 60

AATA 64

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCTTATTAC TGTGAGCCT GCGCGTTCTC CAAGGTTTTC AGATAGAAGG TCAGTTTACG 60

ACGG 64

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
1 5 10 15

Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro
20 25 30

Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile
35 40 45

Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg
50 55 60

Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys

65	70	75	80
Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His			
85	90	95	
Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu			
100	105	110	
Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln			
115	120	125	

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATGGCTAAC TGCTCTAACA TGAT

24

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGATCATGTT AGAGCAGTTA GC

22

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
1 5 10 15
Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp
20 25 30

Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
35 40 45

Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser
50 55 60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65 70 75 80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
85 90 95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Met Ile Thr Leu Arg Lys Leu Pro Leu Ala Val Ala Val Ala Ala
1 5 10 15

Gly Val Met Ser Ala Gln Ala Met Ala Asn Cys
20 25

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Lys, Gly, Asp, Met, Gln, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 18
 - (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 19
 - (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met, Phe, Ile, Arg, Gly, Ala, or Cys"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 20
 - (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 21
 - (D) OTHER INFORMATION: /note= "Xaa at position 21 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser, or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 22
 - (D) OTHER INFORMATION: /note= "Xaa at position 22 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 23
 - (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Val, Ala, Leu, Gly, Trp, Lys, Phe, Ser, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 24
 - (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile, Gly, Val, Arg, Ser, Phe, or Leu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 25
 - (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr, His, Gly, Gln, Arg, Pro, or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 26
 - (D) OTHER INFORMATION: /note= "Xaa at position 26 is His, Thr, Phe, Gly, Arg, Ala, or Trp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 27
 - (D) OTHER INFORMATION: /note= "Xaa at position 27 is Leu, Gly, Arg, Thr, Ser, or Ala"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 28
 (D) OTHER INFORMATION: /note= "Xaa at position 28 is Lys, Arg, Leu, Gln, Gly, Pro, Val, or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 29
 (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln, Asn, Leu, Pro, Arg, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 30
 (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro, His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 31
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 32
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu, Val, Arg, Gln, Asn, Gly, Ala, or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 33
 (D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro, Leu, Gln, Ala, Thr, or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 34
 (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe, Ile, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 35
 (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu, Ala, Gly, Asn, Pro, Gln, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 36
 (D) OTHER INFORMATION: /note= "Xaa at position 36 is Asp, Leu, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 37
 (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe, Ser, Pro, Trp, or Ile"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 38
 (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn,
 or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 40
 (D) OTHER INFORMATION: /note= "Xaa at position 40 is Leu,
 Trp, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 41
 (D) OTHER INFORMATION: /note= "Xaa at position 41 is Asn,
 Cys, Arg, Leu, His, Met, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 42
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,
 Asp, Ser, Cys, Asn, Lys, Thr, Leu, Val, Glu, Phe, Tyr,
 Ile, Met, or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 43
 (D) OTHER INFORMATION: /note= "Xaa at position 43 is Glu,
 Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr, Gly,
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 44
 (D) OTHER INFORMATION: /note= "Xaa at position 44 is Asp,
 Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln, Ala,
 or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 45
 (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,
 Pro, Phe, Val, Met, Leu, Thr, Lys, Trp, Asp, Asn, Arg,
 Ser, Ala, Ile, Glu, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 46
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,
 Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala, Tyr,
 Ile, Val, or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 47
 (D) OTHER INFORMATION: /note= "Xaa at position 47 is Ile,
 Gly, Val, Ser, Arg, Pro, or His"
- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /note= "Xaa at position 48 is Leu, Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala, Met, Val, or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 49
- (D) OTHER INFORMATION: /note= "Xaa at position 49 is Met, Arg, Ala, Gly, Pro, Asn, His, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 50
- (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu, Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val, His, Phe, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 51
- (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 52
- (D) OTHER INFORMATION: /note= "Xaa at position 52 is Asn, His, Arg, Leu, Gly, Ser, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 53
- (D) OTHER INFORMATION: /note= "Xaa at position 53 is Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 54
- (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg, Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His, Ala, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 55
- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Thr, Val, Ser, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 56
- (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr, Phe, Leu, Val, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 57
- (D) OTHER INFORMATION: /note= "Xaa at position 57 is Asn"

or Gly"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 58
 (D) OTHER INFORMATION: /note= "Xaa at position 58 is Leu,
 Ser, Asp, Arg, Gln, Val, or Cys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 59
 (D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu,
 Tyr, His, Leu, Pro, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 60
 (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala,
 Ser, Pro, Tyr, Asn, or Thr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 61
 (D) OTHER INFORMATION: /note= "Xaa at position 61 is Phe,
 Asn, Glu, Pro, Lys, Arg, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 62
 (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn,
 His, Val, Arg, Pro, Thr, Asp, or Ile"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 63
 (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg,
 Tyr, Trp, Lys, Ser, His, Pro, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 64
 (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala,
 Asn, Pro, Ser, or Lys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 65
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val,
 Thr, Pro, His, Leu, Phe, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 66
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys,
 Ile, Arg, Val, Asn, Glu, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 67
 (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser,
 Ala, Phe, Val, Gly, Asn, Ile, Pro, or His"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 68
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Val, Trp, Ser, Ile, Phe, Thr, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 69
 (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 70
 (D) OTHER INFORMATION: /note= "Xaa at position 70 is Asn, Leu, Val, Trp, Pro, or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 71
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala, Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 72
 (D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser, Glu, Met, Ala, His, Asn, Arg, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 73
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala, Glu, Asp, Leu, Ser, Gly, Thr, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 74
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ile, Met, Thr, Pro, Arg, Gly, or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 75
 (D) OTHER INFORMATION: /note= "Xaa at position 75 is Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 76
 (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser, Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 77
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile, Ser, Arg, Thr, or Leu"

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(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 78
  (D) OTHER INFORMATION: /note= "Xaa at position 78 is Leu,
    Ala, Ser, Glu, Phe, Gly, or Arg"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 79
  (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys, Thr,
    Asn, Met, Arg, Ile, Gly, or Asp"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 80
  (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn,
    Trp, Val, Gly, Thr, Leu, Glu, or Arg"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 81
  (D) OTHER INFORMATION: /note= "Xaa at position 81 is Leu,
    Gln, Gly, Ala, Trp, Arg, Val, or Lys"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 82
  (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,
    Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala,
    Tyr, Phe, Ile, Met, or Val"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 83
  (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro,
    Ala, Thr, Trp, Arg, or Met"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 84
  (D) OTHER INFORMATION: /note= "Xaa at position 84 is Cys,
    Glu, Gly, Arg, Met, or Val"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 85
  (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu,
    Asn, Val, or Gln"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 86
  (D) OTHER INFORMATION: /note= "Xaa at position 86 is Pro,
    Cys, Arg, Ala, or Lys"

(ix) FEATURE:
  (A) NAME/KEY: Modified-site
  (B) LOCATION: 87
  (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu,
    Ser, Trp, or Gly"
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- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 88
 (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala,
 Lys, Arg, Val, or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 89
 (D) OTHER INFORMATION: /note= "Xaa at position 89 is Thr,
 Asp, Cys, Leu, Val, Glu, His, Asn, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 90
 (D) OTHER INFORMATION: /note= "Xaa at position 90 is Ala,
 Pro, Ser, Thr, Gly, Asp, Ile, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 91
 (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala,
 Pro, Ser, Thr, Phe, Leu, Asp, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 92
 (D) OTHER INFORMATION: /note= "Xaa at position 92 is Pro,
 Phe, Arg, Ser, Lys, His, Ala, Gly, Ile, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 93
 (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,
 Asp, Ser, Asn, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 94
 (D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,
 Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 95
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is His,
 Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala,
 Trp, Phe, Ile, or Tyr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 96
 (D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro,
 Lys, Tyr, Gly, Ile, or Thr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 97
 (D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile,
 Val, Lys, Ala, or Asn"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 98
 (D) OTHER INFORMATION: /note= "Xaa at position 98 is His,
 Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met,
 Val, Lys, Arg, Tyr, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 99
 (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile,
 Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe,
 or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 100
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is
 Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 101
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is
 Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser,
 Ala, Gly, Ile, Leu, or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 102
 (D) OTHER INFORMATION: /note= "Xaa at position 102 is Gly,
 Leu, Glu, Lys, Ser, Tyr, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 103
 (D) OTHER INFORMATION: /note= "Xaa at position 103 is Asp,
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 104
 (D) OTHER INFORMATION: /note= "Xaa at position 104 is
 Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys, Ala,
 Phe, or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 105
 (D) OTHER INFORMATION: /note= "Xaa at position 105 is
 Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys, Ile,
 Asp, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 106
 (D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu,
 Ser, Ala, Lys, Thr, Ile, Gly, or Pro"
- (ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 108
 (D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg,
 Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala, or Pro"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 109
 (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,
 Thr, Pro, Glu, Tyr, Leu, Ser, or Gly"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 110
 (D) OTHER INFORMATION: /note= "Xaa at position 110 is Lys,
 Ala, Asn, Thr, Leu, Arg, Gln, His, Glu, Ser,
 or Trp"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 111
 (D) OTHER INFORMATION: /note= "Xaa at position 111 is Leu,
 Ile, Arg, Asp, or Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 112
 (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr,
 Val, Gln, Tyr, Glu, His, Ser, or Phe"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 113
 (D) OTHER INFORMATION: /note= "Xaa at position 113 is Phe,
 Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile, Val,
 or Asn"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 114
 (D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr,
 Cys, His, Ser, Trp, Arg, or Leu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 115
 (D) OTHER INFORMATION: /note= "Xaa at position 115 is
 Leu, Asn, Val, Pro, Arg, Ala, His, Thr, Trp, or
 Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 116
 (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,
 Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp, Ser,
 Asn, His, Ala, Tyr, Phe, Glu, or Ile"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 117
 (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr,

Ser, Asn, Ile, Trp, Lys, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 118
- (D) OTHER INFORMATION: /note= "Xaa at position 118 is Leu, Ser, Pro, Ala, Glu, Cys, Asp, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 119
- (D) OTHER INFORMATION: /note= "Xaa at position 119 is Glu, Ser, Lys, Pro, Leu, Thr, Tyr, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 120
- (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Ala, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 123
- (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				20					25					30	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				35					40					45	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				50					55					60	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
65														75	80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				85										95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Xaa	Xaa

100	105	110
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gln Gln Thr Thr Leu		
115	120	125
Ser Leu Ala Ile Phe		
130		

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Gly, Asp, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, Leu, Ile, Phe, Arg, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met, Phe, Ile, Arg, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /note; "Xaa at position 21 is Asp or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Val, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 24
- (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,
Val, Phe, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr,
His, Gly, Gln, Arg, Pro, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /note= "Xaa at position 26 is His,
Phe, Gly, Arg, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /note= "Xaa at position 28 is Lys,
Leu, Gln, Gly, Pro, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,
Asn, Leu, Arg, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro,
His, Thr, Gly, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro,
Asp, Gly, Ala, Arg, Leu, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /note= "Xaa at position 32 Leu,
Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 33
- (D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro,
Leu, Gln, Ala, or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 34
- (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,
Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe,
Thr, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 35
(D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu,
Ala, Asn, Pro, Gln, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 36
(D) OTHER INFORMATION: /note= "Xaa at position 36 is Asp
or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 37
(D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,
Ser, Pro, Trp, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 38
(D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn
or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 41
(D) OTHER INFORMATION: /note= "Xaa at position 41 is Asn,
Cys, Arg, His, Met, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 42
(D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,
Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, Val,
or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 44
(D) OTHER INFORMATION: /note="Xaa at position 44 is Asp or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 45
(D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,
Val, Met, Leu, Thr, Lys, Ala, Asn, Glu, Ser, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 46
(D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,
Phe, Ser, Thr, Cys, Ala, Asn, Gln, Glu, His, Ile, Lys,
Tyr, Val, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 47
(D) OTHER INFORMATION: /note= "Xaa at position 47 is Ile, Val,
or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 49
 - (D) OTHER INFORMATION: /note= "Xaa at position 49 is Met, Asn, or Asp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 50
 - (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu, Thr, Ala, Asn, Ser, or Asp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 51
 - (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, Met, Pro, Ser, Thr, or His"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 52
 - (D) OTHER INFORMATION: /note= "Xaa at position 52 is Asn or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 53
 - (D) OTHER INFORMATION: /note= "Xaa at position 53 is Leu, Met, or Phe"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 54
 - (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg Ala, or Ser"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 55
 - (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Thr, Val, Leu, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 56
 - (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Cys, Ser, Gln, Ala, Arg, Asn, Glu, His, Leu, Thr, Val, or Lys"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 59
 - (D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu, Tyr, His, Leu, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 60
 - (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala, Ser, Asn, or Thr"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site

(B) LOCATION: 61
 (D) OTHER INFORMATION: /note= "Xaa at position 61 is Phe or Ser"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 62
 (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, Val, Pro, Thr, or Ile"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 63
 (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg, Tyr, Lys, Ser, His, or Val"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 64
 (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala or Asn"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 65
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val, Thr, Leu, or Ser"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 66
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys, Ile, Arg, Val, Asn, Glu, or Ser"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 67
 (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser, Phe, Val, Gly, Asn, Ile, or His"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 68
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Val, Ile, Phe, or His"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 69
 (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln, Ala, Pro, Thr, Glu, Arg, or Gly"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 70
 (D) OTHER INFORMATION: /note= "Xaa at position 70 is Asn or Pro"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 71

(D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala,
Met, Pro, Arg, Glu, Thr, or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 72
 (D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser,
Glu, Met, Ala, His, Asn, Arg, or Asp"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 73
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala,
Glu, Asp, Leu, Ser, Gly, Thr, Arg, or Pro"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 74
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ile
or Met"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 75
 (D) OTHER INFORMATION: /note= "Xaa at position 75 is Glu,
Gly, Asp, Ser, or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 76
 (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,
Val, Ala, Asn, Glu, Pro, Gly, or Asp"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 77
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile,
Ser, or Leu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 79
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys,
Thr, Asn, Met, Arg, Ile, Gly, or Asp"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 80
 (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn,
Val, Gly, Thr, Leu, Glu, or Arg"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 81
 (D) OTHER INFORMATION: /note= "Xaa at position 81 is Leu
or Val"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 82
 (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,

Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Met, Phe,
Ser, Thr, Tyr, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 83
- (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro,
Ala, Thr, Trp, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 85
- (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu
or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 87
- (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu
or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 88
- (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala,
Arg, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 89
- (D) OTHER INFORMATION: /note= "Xaa at position 89 is Thr,
Asp, Glu, His, Asn, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 90
- (D) OTHER INFORMATION: /note= "Xaa at position 90 is Ala,
Asp, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 91
- (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala,
Pro, Ser, Thr, Phe, Leu, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 92
- (D) OTHER INFORMATION: /note= "Xaa at position 92 is Pro
or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 93
- (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,
Asp, Ser, Pro, Ala, Leu, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 95
- (D) OTHER INFORMATION: /note= "Xaa at position 95 is His,

Pro, Arg, Val, Leu, Gly, Asn, Ile, Phe, Ser,
or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 96
- (D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro
or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 97
- (D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile,
Val, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 98
- (D) OTHER INFORMATION: /note= "Xaa at position 98 is His,
Ile, Asn, Leu, Asp, Ala, Thr, Arg, Gln, Glu,
Lys, Met, Ser, Tyr, Val, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 99
- (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile,
Leu, Val, or Phe"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 100
- (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys,
Leu, His, Arg, Ile, Gln, Pro, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 101
- (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp,
Pro, Met, Lys, His, Thr, Val, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 102
- (D) OTHER INFORMATION: /note= "Xaa at position 102 is Gly,
Glu, Lys, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 104
- (D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp,
Val, Tyr, Met, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 105
- (D) OTHER INFORMATION: /note= "Xaa at position 105 is
Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys,
Ile, Asp or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 106
(D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu,
Ser, Ala, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 108
(D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg,
Ala, Gln, Ser, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 109
(D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,
Thr, Glu, Leu, Ser, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 112
(D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr,
Val, Gln, Glu, His, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 114
(D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr
or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 115
(D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu
or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 116
(D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,
Thr, Met, Val, Trp, Ser, Leu, Ala, Asn, Gln, His, Phe,
Tyr, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 117
(D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr,
Ser, or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 119
(D) OTHER INFORMATION: /note= "Xaa at position 119 is
Glu, Ser, Pro, Leu, Thr, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
(B) LOCATION: 120
(D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn,
Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

(B) LOCATION: 121
 (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 122
 (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 123
 (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa
				20				25					30		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Leu
				35			40					45			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				50			55			60					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa
				65			70			75				80	
Xaa	Xaa	Xaa	Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa
			85					90					95		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Lys	Leu	Xaa
				100				105					110		
Phe	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu
				115				120					125		
Ser	Leu	Ala	Ile	Phe											
				130											

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 1
 (D) OTHER INFORMATION: /note= "Met- may or may not precede"

the amino acid in position 1"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 17
 (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser,
 Gly, Asp, Met, or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 18
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn,
 His, or Ile"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 19
 (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met
 or Ile"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 21
 (D) OTHER INFORMATION: /note= "Xaa at position 21 is Asp
 or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 23
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile,
 Ala, Leu, or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 24
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Ile,
 Val, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 25
 (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr,
 His, Gln, or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 26
 (D) OTHER INFORMATION: /note= "Xaa at position 26 is His
 or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 29
 (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,
 Asn, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 30
 (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro,
 Gly, or Gln"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 31
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Pro, Asp, Gly, or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 32
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu, Arg, Gln, Asn, Gly, Ala, or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 33
 (D) OTHER INFORMATION: /note= "Xaa at position 33 is Pro or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 34
 (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe Thr, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 35
 (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu, Ala, Asn, Pro, Gln, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 37
 (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe, Ser, Pro, or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 38
 (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 42
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly, Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 44
 (D) OTHER INFORMATION: /note= "Xaa at position 44 is Asp or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 45
 (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln, Val, Met, Leu, Thr, Ala, Asn, Glu, Ser, or Lys"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 46
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp,
 Phe, Ser, Thr, Ala, Asn, Gln, Glu, His, Ile, Lys,
 Tyr, Val, or Cys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 50
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu,
 Ala, Asn, Ser, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 51
 (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn,
 Arg, Met, Pro, Ser, Thr, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 54
 (D) OTHER INFORMATION: /note= "Xaa at position 54 is Arg
 or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 55
 (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg,
 Thr, Val, Leu, or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 56
 (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro,
 Gly, Ser, Gln, Ala, Arg, Asn, Glu, Leu, Thr, Val,
 or Lys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 60
 (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 62
 (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn,
 Pro, Thr, or Ile"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 63
 (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg
 or Lys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 64
 (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala

or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 65
- (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val
or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 66
- (D) OTHER INFORMATION: /note= "Xaa at position 66 is Lys
or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 67
- (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser
Phe or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 68
- (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
Ile, Phe, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 69
- (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln,
Ala, Pro, Thr, Glu, Arg, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 71
- (D) OTHER INFORMATION: /note= "Xaa at position 71 is Ala,
Pro, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 72
- (D) OTHER INFORMATION: /note= "Xaa at position 72 is Ser,
Glu, Arg, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 73
- (D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala
or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 76
- (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,
Val, Ala, Asn, Glu, Pro, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 77
- (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile
or Leu"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 79
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is
 Lys, Thr, Asn, Met, Arg, Ile, Gly, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 80
 (D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn,
 Gly, Glu, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 82
 (D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,
 Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Ile, Met,
 Phe, Ser, Thr, Tyr, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 83
 (D) OTHER INFORMATION: /note= "Xaa at position 83 is Pro
 or Thr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 85
 (D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu
 or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 87
 (D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 88
 (D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala
 or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 91
 (D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala
 or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 93
 (D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,
 Asp, Ser, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 95
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is His,
 Pro, Arg, Val, Leu, Gly, Asn, Phe, Ser, or Thr"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 96
 (D) OTHER INFORMATION: /note= "Xaa at position 96 is Pro or Tyr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 97
 (D) OTHER INFORMATION: /note= "Xaa at position 97 is Ile or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 98
 (D) OTHER INFORMATION: /note= "Xaa at position 98 is His, Ile, Asn, Leu, Ala, Thr, Arg, Gln, Lys, Met, Ser, Tyr, Val, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 99
 (D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile, Leu, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 100
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys, Arg, Ile, Gln, Pro, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 101
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp, Pro, Met, Lys, His, Thr, Pro, Asn, Ile, Leu, or Tyr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 104
 (D) OTHER INFORMATION: /note= "Xaa at position 104 is Trp or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 105
 (D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn, Pro, Ala, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 106
 (D) OTHER INFORMATION: /note= "Xaa at position 106 is Glu or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 109
 (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,

Thr, Glu, Leu, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 112
- (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 114
- (D) OTHER INFORMATION: /note= "Xaa at position 114 is Tyr or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 115
- (D) OTHER INFORMATION: /note= "Xaa at position 115 is Leu or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 116
- (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys, Thr, Val, Trp, Ser, Ala, His, Met, Phe, Tyr, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 117
- (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 120
- (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Asn, Pro, Asp, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 123
- (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn Cys

1	5	10	15
Xaa Xaa Xaa Ile Xaa Glu Xaa Xaa Xaa Xaa Leu Lys Xaa Xaa Xaa Xaa	20	25	30
Xaa Xaa Xaa Asp Xaa Xaa Asn Leu Asn Xaa Glu Xaa Xaa Xaa Ile Leu	35	40	45
Met Xaa Xaa Asn Leu Xaa Xaa Xaa Asn Leu Glu Xaa Phe Xaa Xaa Xaa	50	55	60
Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Ile Glu Xaa Xaa Leu Xaa Xaa	65	70	75
Leu Xaa Xaa Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg Xaa Xaa	85	90	95
Xaa Xaa Xaa Xaa Xaa Gly Asp Xaa Xaa Xaa Phe Xaa Xaa Lys Leu Xaa	100	105	110
Phe Xaa Xaa Xaa Xaa Leu Glu Xaa Xaa Xaa Xaa Gln Gln Thr Thr Leu	115	120	125
Ser Leu Ala Ile Phe	130		

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Ser, Gly, Asp, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr, His, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 26
- (D) OTHER INFORMATION: /note= "Xaa at position 26 is His or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /note= "Xaa at position 30 is Pro or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu, Arg, Asn, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 34
- (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu, Val, Ser, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION: /note= "Xaa at position 35 is Leu, Ala, Asn, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 38
- (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 42
- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly, Asp, Ser, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 45
- (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln, Val, Met, Leu, Ala, Asn, Glu, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 46
- (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp, Phe, Ser, Gln, Glu, His, Val, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 50
- (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu, Asn, Ser, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 51
- (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, Pro, Thr, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 55
- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 56
- (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro, Gly, Ser, Ala, Asn, Val, Leu, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 62
- (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn, Pro, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 64
- (D) OTHER INFORMATION: /note= "Xaa at position 64 is Ala or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 65
- (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 67
- (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser or Phe"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 68
- (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu or Phe"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 69

(D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln,
Ala, Glu, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 76

(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,
Val, Asn, Pro, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 77

(D) OTHER INFORMATION: /note= "Xaa at position 77 is Ile
or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 79

(D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys,
Asn, Met, Arg, Ile, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 80

(D) OTHER INFORMATION: /note= "Xaa at position 80 is Asn,
Gly, Glu, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 82

(D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,
Gln, Trp, Arg, Asp, Asn, Glu, His, Met, Phe, Ser,
Thr, Tyr, or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 87

(D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 88

(D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala
or Trp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 91

(D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala
or Pro"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 93

(D) OTHER INFORMATION: /note= "Xaa at position 93 is Thr,
Asp, or Ala"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 95

(D) OTHER INFORMATION: /note= "Xaa at position 95 is His,
Pro, Arg, Val, Gly, Asn, Ser, or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 98

(D) OTHER INFORMATION: /note= "Xaa at position 98 is His,
Ile, Asn, Ala, Thr, Arg, Gln, Glu, Lys, Met, Ser,
Tyr, Val, or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 99

(D) OTHER INFORMATION: /note= "Xaa at position 99 is Ile
or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 100

(D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys
or Arg"

(ix) FEATURE;

(A) NAME/KEY: Modified-site

(B) LOCATION: 101

(D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp,
Pro, Met, Lys, Thr, His, Pro, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 105

(D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn,
Pro, Ser, Ile, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 108

(D) OTHER INFORMATION: /note= "Xaa at position 108 is Arg, Ala,
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 109

(D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,
Thr, Glu, Leu, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 112

(D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr
or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 116

(D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,
Val, Trp, Ala, His, Phe, Tyr, or Ile"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 117

(D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr

or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 120
- (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 121
- (D) OTHER INFORMATION: /note= "Xaa at position 121 is Ala, Ser, Ile, Pro, or Asp"s

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 122
- (D) OTHER INFORMATION: /note= "Xaa at position 122 is Gln, Met, Trp, Phe, Pro, His, Ile, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 123
- (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala, Met, Glu, Ser, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	
Xaa	Xaa	Met	Ile	Asp	Glu	Xaa	Ile	Xaa	Xaa	Leu	Lys	Xaa	Xaa	Pro	Xaa
			20					25						30	
Pro	Xaa	Xaa	Asp	Phe	Xaa	Asn	Leu	Asn	Xaa	Glu	Asp	Xaa	Xaa	Ile	Leu
			35				40					45			
Met	Xaa	Xaa	Asn	Leu	Arg	Xaa	Xaa	Asn	Leu	Glu	Ala	Phe	Xaa	Arg	Xaa
			50				55				60				
Xaa	Lys	Xaa	Xaa	Xaa	Asn	Ala	Ser	Ala	Ile	Glu	Xaa	Xaa	Leu	Xaa	Xaa
	65				70					75				80	
Leu	Xaa	Pro	Cys	Leu	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg	Xaa	Pro
			85					90						95	
Ile	Xaa	Xaa	Xaa	Xaa	Gly	Asp	Trp	Xaa	Glu	Phe	Xaa	Xaa	Lys	Leu	Xaa
			100					105					110		
Phe	Tyr	Leu	Xaa	Xaa	Leu	Glu	Xaa	Xaa	Xaa	Xaa	Gln	Gln	Thr	Thr	Leu
		115					120					125			
Ser	Leu	Ala	Ile	Phe											
			130												

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 1
 - (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 3
 - (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Lys, Gly, Asp, Met, Gln, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 4
 - (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, Leu, Ile, Phe, Arg, or Gln"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 5
 - (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met, Phe, Ile, Arg, Gly, Ala, or Cys"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 6
 - (D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile, Cys, Gln, Glu, Arg, Pro, or Ala"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 7
 - (D) OTHER INFORMATION: /note= "Xaa at position 7 is Asp, Phe, Lys, Arg, Ala, Gly, Glu, Gln, Asn, Thr, Ser, or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 8
 - (D) OTHER INFORMATION: /note= "Xaa at position 8 is Glu, Trp, Pro, Ser, Ala, His, Asp, Asn, Gln, Leu, Val, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 9
 - (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Val, Ala, Leu, Gly, Trp, Lys, Phe, Ser or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 10
 - (D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile, Gly, Val, Arg, Ser, Phe, or Leu"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr,
 His, Gly, Gln, Arg, Pro, or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 12
 (D) OTHER INFORMATION: /note= "Xaa at position 12 is His,
 Thr, Phe, Gly, Arg, Ala, or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 13
 (D) OTHER INFORMATION: /note= "Xaa at position 13 is Leu,
 Gly, Arg, Thr, Ser, or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 14
 (D) OTHER INFORMATION: /note= "Xaa at position 14 is Lys,
 Arg, Leu, Gln, Gly, Pro, Val, or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 15
 (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln,
 Asn, Leu, Pro, Arg, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 16
 (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro,
 His, Thr, Gly, Asp, Gln, Ser, Leu, or Lys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 17
 (D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro,
 Asp, Gly, Ala, Arg, Leu, or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 18
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,
 Val, Arg, Gln, Asn, Gly, Ala, or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 19
 (D) OTHER INFORMATION: /note= "Xaa at position 19 is Pro,
 Leu, Gln, Ala, Thr, or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 20
 (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu,
 Val, Gly, Ser, Lys, Glu, Gln, Thr, Arg, Ala, Phe,
 Ile, or Met"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 21
 (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu,
 Ala, Gly, Asn, Pro, Gln, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 22
 (D) OTHER INFORMATION: /note= "Xaa at position 22 is Asp,
 Leu, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 23
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,
 Ser, Pro, Trp, or Ile"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 24
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn
 or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 26
 (D) OTHER INFORMATION: /note= "Xaa at position 26 is Leu,
 Trp, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 27
 (D) OTHER INFORMATION: /note= "Xaa at position 27 is Asn,
 Cys, Arg, Leu, His, Met, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 28
 (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,
 Asp, Ser, Cys, Ala, Lys, Asn, Thr, Leu, Val, Glu,
 Phe, Tyr, Ile, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 29
 (D) OTHER INFORMATION: /note= "Xaa at position 29 is Glu,
 Asn, Tyr, Leu, Phe, Asp, Ala, Cys, Gln, Arg, Thr,
 Gly, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 30
 (D) OTHER INFORMATION: /note= "Xaa at position 30 is Asp,
 Ser, Leu, Arg, Lys, Thr, Met, Trp, Glu, Asn, Gln,
 Ala, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 31
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,

Pro, Phe, Val, Met, Leu, Thr, Lys, Asp, Asn, Arg,
Ser, Ala, Ile, Glu, His, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,
Phe, Ser, Thr, Cys, Glu, Asn, Gln, Lys, His, Ala,
Tyr, Ile, Val, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 33
- (D) OTHER INFORMATION: /note= "Xaa at position 33 is Ile,
Gly, Val, Ser, Arg, Pro, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 34
- (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu,
Ser, Cys, Arg, Ile, His, Phe, Glu, Lys, Thr, Ala,
Met, Val, or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION: /note= "Xaa at position 35 is Met,
Arg, Ala, Gly, Pro, Asn, His, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 36
- (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu,
Leu, Thr, Asp, Tyr, Lys, Asn, Ser, Ala, Ile, Val,
His, Phe, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,
Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 38
- (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn,
His, Arg, Leu, Gly, Ser, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 39
- (D) OTHER INFORMATION: /note= "Xaa at position 39 is
Leu, Thr, Ala, Gly, Glu, Pro, Lys, Ser, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 40
- (D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg,
Asp, Ile, Ser, Val, Thr, Gln, Asn, Lys, His,
Ala, or Leu"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 41
 (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,
 Thr, Val, Ser, Leu, or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 42
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro,
 Gly, Cys, Ser, Gln, Glu, Arg, His, Thr, Ala, Tyr,
 Phe, Leu, Val, or Lys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 43
 (D) OTHER INFORMATION: /note= "Xaa at position 43 is Asn
 or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 44
 (D) OTHER INFORMATION: /note= "Xaa at position 44 is Leu,
 Ser, Asp, Arg, Gln, Val, or Cys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 45
 (D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu,
 Tyr, His, Leu, Pro, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 46
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala,
 Ser, Pro, Tyr, Asn, or Thr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 47
 (D) OTHER INFORMATION: /note= "Xaa at position 47 is Phe,
 Asn, Glu, Pro, Lys, Arg, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 48
 (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,
 His, Val, Arg, Pro, Thr, Asp, or Ile"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 49
 (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg,
 Tyr, Trp, Lys, Ser, His, Pro, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 50
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala,
 Asn, Pro, Ser, or Lys"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 51
 (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val,
 Thr, Pro, His, Leu, Phe, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 52
 (D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys,
 Ile, Arg, Val, Asn, Glu, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 53
 (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,
 Ala, Phe, Val, Gly, Asn, Ile, Pro, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 54
 (D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu,
 Val, Trp, Ser, Ile, Phe, Thr, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 55
 (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,
 Ala, Pro, Thr, Glu, Arg, Trp, Gly, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 56
 (D) OTHER INFORMATION: /note= "Xaa at position 56 is Asn,
 Leu, Val, Trp, Pro, or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 57
 (D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala,
 Met, Leu, Pro, Arg, Glu, Thr, Gln, Trp, or Asn"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 58
 (D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser,
 Glu, Met, Ala, His, Asn, Arg, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 59
 (D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala,
 Glu, Asp, Leu, Ser, Gly, Thr, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 60
 (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ile,
 Met, Thr, Pro, Arg, Gly, Ala"
- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 61
 - (D) OTHER INFORMATION: /note= "Xaa at position 61 is
Glu, Lys, Gly, Asp, Pro, Trp, Arg, Ser, Gln,
or Leu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 62
 - (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,
Val, Ala, Asn, Trp, Glu, Pro, Gly, or Asp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 63
 - (D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile,
Ser, Arg, Thr, or Leu"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 64
 - (D) OTHER INFORMATION: /note= "Xaa at position 64 is Leu,
Ala, Ser, Glu, Phe, Gly, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 65
 - (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,
Thr, Gly, Asn, Met, Arg, Ile, or Asp"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 66
 - (D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,
Trp, Val, Gly, Thr, Leu, Glu, or Arg"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 67
 - (D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu,
Gln, Gly, Ala, Trp, Arg, Val, or Lys"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 68
 - (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
Gln, Lys, Trp, Arg, Asp, Glu, Asn, His, Thr, Ser, Ala,
Tyr, Phe, Ile, Met, or Val"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 69
 - (D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro,
Ala, Thr, Trp, Arg, or Met"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 70
 - (D) OTHER INFORMATION: /note= "Xaa at position 70 is Cys,
Glu, Gly, Arg, Met, or Val"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 71
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu, Asn, Val, or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 72
 (D) OTHER INFORMATION: /note= "Xaa at position 72 is Pro, Cys, Arg, Ala, or Lys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 73
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu, Ser, Trp, or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 74
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala, Lys, Arg, Val, or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 75
 (D) OTHER INFORMATION: /note= "Xaa at position 75 is Thr, Asp, Cys, Leu, Val, Glu, His, Asn, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 76
 (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ala, Pro, Ser, Thr, Gly, Asp, Ile, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 77
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala, Pro, Ser, Thr, Phe, Leu, Asp, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 78
 (D) OTHER INFORMATION: /note= "Xaa at position 78 is Pro, Phe, Arg, Ser, Lys, His, Ala, Gly, Ile, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 79
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr, Asp, Ser, Asn, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 80
 (D) OTHER INFORMATION: /note= "Xaa at position 80 is Arg, Ile, Ser, Glu, Leu, Val, Gln, Lys, His, Ala, or Pro"
- (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 81
- (D) OTHER INFORMATION: /note= "Xaa at position 81 is His, Gln, Pro, Arg, Val, Leu, Gly, Thr, Asn, Lys, Ser, Ala, Trp, Phe, Ile, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 82
- (D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro, Lys, Tyr, Gly, Ile, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 83
- (D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile, Val, Lys, Ala, or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 84
- (D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Leu, Asp, Ala, Thr, Glu, Gln, Ser, Phe, Met, Val, Lys, Arg, Tyr, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 85
- (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile, Leu, Arg, Asp, Val, Pro, Gln, Gly, Ser, Phe, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 86
- (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys, Tyr, Leu, His, Arg, Ile, Ser, Gln, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 87
- (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Pro, Met, Lys, His, Thr, Val, Tyr, Glu, Asn, Ser, Ala, Gly, Ile, Leu, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 88
- (D) OTHER INFORMATION: /note= "Xaa at position 88 Gly, Leu, Glu, Lys, Ser, Tyr, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 89
- (D) OTHER INFORMATION: /note= "Xaa at position 89 is Asp or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 90
- (D) OTHER INFORMATION: /note= "Xaa at position 90 is

Trp, Val, Cys, Tyr, Thr, Met, Pro, Leu, Gln, Lys,
Ala, Phe, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 91
- (D) OTHER INFORMATION: /note= "Xaa at position 91 is
Asn, Pro, Ala, Phe, Ser, Trp, Gln, Tyr, Leu, Lys,
Ile, Asp, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 92
- (D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu,
Ser, Ala, Lys, Thr, Ile, Gly, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 94
- (D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,
Lys, Asp, Leu, Thr, Ile, Gln, His, Ser, Ala, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 95
- (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,
Thr, Pro, Glu, Tyr, Leu, Ser, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 96
- (D) OTHER INFORMATION: /note= "Xaa at position 96 is Lys,
Asn, Thr, Leu, Gln, Arg, His, Glu, Ser, Ala,
or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 97
- (D) OTHER INFORMATION: /note= "Xaa at position 97 is Leu,
Ile, Arg, Asp, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 98
- (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr,
Val, Gln, Tyr, Glu, His, Ser, or Phe"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 99
- (D) OTHER INFORMATION: /note= "Xaa at position 99 is Phe,
Ser, Cys, His, Gly, Trp, Tyr, Asp, Lys, Leu, Ile,
Val, or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 100
- (D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr,
Cys, His, Ser, Trp, Arg, or Leu"

(ix) FEATURE:

1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399</
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(A) NAME/KEY: Modified-site
(B) LOCATION: 102
(D) OTHER INFORMATION: /note= "Xaa at position 102 is
Lys, Leu, Pro, Thr, Met, Asp, Val, Glu, Arg, Trp,
Ser, Asn, His, Ala, Tyr, Phe, Gln, or Ile"

(A) NAME/KEY: Modified-site
(B) LOCATION: 103
(D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr,
Ser, Asn, Ile, Trp, Lys, or Pro"

(A) NAME/KEY: Modified-site
(B) LOCATION: 104
(D) OTHER INFORMATION: /note= "Xaa at position 104 is Leu,
Ser, Pro, Ala, Glu, Cys, Asp, or Tyr"

(A) NAME/KEY: Modified-site
(B) LOCATION: 105
(D) OTHER INFORMATION: /note= "Xaa at position 105 is Glu,
Ser, Lys, Pro, Leu, Thr, Tyr, or Arg"

(A) NAME/KEY: Modified-site
(B) LOCATION: 106
(D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,
Ala, Pro, Leu, His, Val or Gln"

(A) NAME/KEY: Modified-site
(B) LOCATION: 107
(D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala,
Ser, Ile, Asn, Pro, Lys, Asp, or Gly"

(A) NAME/KEY: Modified-site
(B) LOCATION: 108
(D) OTHER INFORMATION: /note= "Xaa at position 108 is
Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr,
or Cys"

(A) NAME/KEY: Modified-site
(B) LOCATION: 109
(D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala,
Met, Glu, His, Ser, Pro, Tyr, or Leu"

Asn Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5 10 15

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	20	25	30
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	35	40	45
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	50	55	60
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	65	70	75
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	85	90	95
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	100	105	110

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Gly, Asp, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, Leu,Ile, Phe, Arg, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met, Phe, Ile, Arg, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7

(D) OTHER INFORMATION: /note= "Xaa at position 7 is Asp or Glu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 9
 (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Val, Ala, Leu, or Gly"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 10
 (D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile, Val, Phe, or Leu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr, His, Gly, Gln, Arg, Pro, or Ala"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 12
 (D) OTHER INFORMATION: /note= "Xaa at position 12 is His, Phe, Gly, Arg, or Ala"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 14
 (D) OTHER INFORMATION: /note= "Xaa at position 14 is Lys, Leu, Gln, Gly, Pro, or Val"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 15
 (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln, Asn, Leu, Arg, or Val"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 16
 (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro, His, Thr, Gly, or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 17
 (D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro, Asp, Gly, Ala, Arg, Leu, or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 18
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Arg, Gln, Asn, Gly, Ala or Glu"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 19
 (D) OTHER INFORMATION: /note= "Xaa at poisiton 19 is Pro, Leu, Gln, Ala, or Glu"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 20
 (D) OTHER INFORMATION: /note= "Xaa at positon 20 is Leu,
 Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe,
 Thr, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 21
 (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu,
 Ala, Asn, Pro, Gln, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 22
 (D) OTHER INFORMATION: /note= "Xaa at position 22 is Asp
 or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 23
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,
 Ser, Pro, Trp, or Ile"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 24
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn
 or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 27
 (D) OTHER INFORMATION: /note= "Xaa at position 27 is Asn,
 Cys, Arg, His, Met, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 28
 (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,
 Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 30
 (C) OTHER INFORMATION: /note= "Xaa at position 30 is Asp
 or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 31
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,
 Val, Met, Leu, Thr, Lys, Ala, Asn, Glu, Ser, or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 32
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,
 Phe, Ser, Thr, Cys, Ala, Asn, Gln, Glu, His, Ile,

Lys, Tyr, Val, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 33
- (D) OTHER INFORMATION: /note= "Xaa at position 33 is Ile, Val, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 35
- (D) OTHER INFORMATION: /note= "Xaa at position 35 is Met, Asn, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 36
- (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu, Thr, Ala, Asn, Ser, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn, Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 38
- (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 39
- (D) OTHER INFORMATION: /note= "Xaa at position 39 is Leu, Met, or Phe"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 40
- (D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg, Ala, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 41
- (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg, Thr, Val, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 42
- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro, Gly, Cys, Ser, Gln, Ala, Arg, Asn, Glu, His, Leu, Thr, Val, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 45
- (D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu,

Tyr, His, Leu, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 46
- (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala, Ser, Asn, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 47
- (D) OTHER INFORMATION: /note= "Xaa at position 47 is Phe or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn, Val, Pro, Thr, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 49
- (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg, Tyr, Lys, Ser, His, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 50
- (D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 51
- (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val, Thr, Leu, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 52
- (D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys, Ile, Arg, Val, Asn, Glu, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 53
- (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser, Phe, Val, Gly, Asn, Ile, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 54
- (D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu, Val, Ile, Phe, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 55
- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln, Ala, Pro, Thr, Glu, Arg, or Gly"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 56
 (D) OTHER INFORMATION: /note= "Xaa at position 56 is Asn
 or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 57
 (D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala,
 Met, Pro, Arg, Glu, Thr, or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 58
 (D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser,
 Glu, Met, Ala, His, Asn, Arg, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 59
 (D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala,
 Glu, Asp, Leu, Ser, Gly, Thr, Arg, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 60
 (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ile
 or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 61
 (D) OTHER INFORMATION: /note= "Xaa at position 61 is Glu,
 Gly, Asp, Ser, or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 62
 (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,
 Val, Ala, Asn, Glu, Pro, Gly, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 63
 (D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile,
 Ser, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 65
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,
 Thr, Gly, Asn, Met, Arg, Ile, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 66
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,
 Val, Gly, Thr, Leu, Glu, or Arg"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 67
 (D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu
 or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 68
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
 Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Met, Phe,
 Ser, Thr, Tyr, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 69
 (D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro,
 Ala, Thr, Trp, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 71
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu
 or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 73
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 74
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala,
 Arg, or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 75
 (D) OTHER INFORMATION: /note= "Xaa at position 75 is Thr,
 Asp, Glu, His, Asn, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 76
 (D) OTHER INFORMATION: /note= "Xaa at position 76 is Ala,
 Asp, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 77
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala,
 Pro, Ser, Thr, Phe, Leu, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 78
 (D) OTHER INFORMATION: /note= "Xaa at position 78 is Pro
 or Ser"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 79
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr, Asp, Ser, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 81
 (D) OTHER INFORMATION: /note= "Xaa at position 81 is His, Pro, Arg, Val, Leu, Gly, Asn, Ile, Phe, Ser, or Thr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 82
 (D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro or Tyr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 83
 (D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile, Val, or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 84
 (D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Leu, Asp, Ala, Thr, Arg, Gln, Glu, Lys, Met, Ser, Tyr, Val, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 85
 (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile, Leu, Val, or Phe"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 86
 (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys, Leu, His, Arg, Ile, Gln, Pro, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 87
 (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Pro, Met, Lys, His, Thr, Val, Asn, Ile, Leu, or Tyr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 88
 (D) OTHER INFORMATION: /note= "Xaa at position 88 is Gly, Glu, Lys, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 90
 (D) OTHER INFORMATION: /note= "Xaa at position 90 is Trp, Val, Tyr, Met, or Leu"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 91
 (D) OTHER INFORMATION: /note=
 "Xaa at position 91 is Asn, Pro, Ala, Phe, Ser,
 Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 92
 (D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu,
 Ser, Ala, or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 94
 (D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,
 Ala, Gln, Ser, or Lys"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 95
 (D) OTHER INFORMATION: /note= "Xaa at position 95 Arg,
 Thr, Glu, Leu, Ser, or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 98
 (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr,
 Val, Gln, Glu, His, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 100
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr
 or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 101
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu
 or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 102
 (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys,
 Thr, Met, Val, Trp, Ser, Leu, Ala, Asn, Gln, His,
 Phe, Tyr, or Ile"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 103
 (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr,
 Ser, or Asn"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 105
 (D) OTHER INFORMATION: /note= "Xaa at position 105 is Glu,
 Ser, Pro, Leu, Thr, or Tyr"

- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 106
 - (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn, Pro, Leu, His, Val, or Gln"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 107
 - (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala, Ser, Ile, Asn, Pro, Lys, Asp, or Gly"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 108
 - (D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln, Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"
- (ix) FEATURE:
- (A) NAME/KEY: Modified-site
 - (B) LOCATION: 109
 - (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala, Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Asn	Cys	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	1	5	10	15
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	20	25	30	
Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Xaa	Xaa	35	40	45	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	50	55	60	
Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Arg	65	70	75	80
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Lys	85	90	95	
Leu	Xaa	Phe	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Gln		100	105	110	

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Gly, Asp, Met, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 7
- (C) OTHER INFORMATION: /note= "Xaa at position 7 is Asp or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /note= "Xaa at position 10 is Ile, Val, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr, His, Gln, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "Xaa at position 12 is His or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln, Asn, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro,

Gly, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /note= "Xaa at position 17 is Pro, Asp, Gly, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Arg, Gln, Asn, Gly, Ala, or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "Xaa at position 19 is Pro or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu, Val, Gly, Ser, Lys, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu, Ala, Asn, Pro, Gln, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe, Ser, Pro, or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly, Asp, Ser, Cys, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 30
- (D) OTHER INFORMATION: /note= "Xaa at position 30 is Asp or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,

Val, Met, Leu, Thr, Ala, Asn, Glu, Ser, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32
- (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,
Phe, Ser, Thr, Ala, Asn, Gln, Glu, His, Ile, Lys,
Tyr, Val, or Cys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 36
- (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu,
Ala, Asn, Ser, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 37
- (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,
Arg, Met, Pro, Ser, Thr, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 40
- (D) OTHER INFORMATION: /note= "Xaa at position 40 is Arg
or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 41
- (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,
Thr, Val, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 42
- (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro,
Gly, Ser, Gln, Ala, Arg, Asn, Glu, Leu, Thr, Val,
or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 46
- (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala
or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 48
- (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,
Pro, Thr, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 49
- (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg
or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 50

(D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala
or Asn"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 51

(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val
or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 52

(D) OTHER INFORMATION: /note= "Xaa at position 52 is Lys
or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 53

(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,
Phe, or His"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 54

(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu,
Ile, Phe, or His"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 55

(D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,
Ala, Pro, Thr, Glu, Arg, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 57

(D) OTHER INFORMATION: /note= "Xaa at position 57 is Ala,
Pro, or Arg"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 58

(D) OTHER INFORMATION: /note= "Xaa at position 58 is Ser,
Glu, Arg, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 59

(D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala
or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 62

(D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,
Val, Ala, Asn, Glu, Pro, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 63

(D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile

or Leu"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 65
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,
 Thr, Gly, Asn, Met, Arg, Ile, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 66
 (D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn,
 Gly, Glu, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 68
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
 Gln, Trp, Arg, Asp, Ala, Asn, Glu, His, Ile, Met,
 Phe, Ser, Thr, Tyr, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 69
 (D) OTHER INFORMATION: /note= "Xaa at position 69 is Pro
 or Thr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 71
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu
 or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 73
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 74
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala
 or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 77
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala
 or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 79
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr,
 Asp, Ser, Pro, Ala, Leu, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 81
 (D) OTHER INFORMATION: /note= "Xaa at position 81 is His,

Pro, Arg, Val, Leu, Gly, Asn, Phe, Ser, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 82
- (D) OTHER INFORMATION: /note= "Xaa at position 82 is Pro or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 83
- (D) OTHER INFORMATION: /note= "Xaa at position 83 is Ile or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 84
- (D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Leu, Ala, Thr, Arg, Gln, Lys, Met, Ser, Tyr, Val, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 85
- (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile, Leu, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 86
- (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys, Arg, Ile, Gln, Pro, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 87
- (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Pro, Met, Lys, His, Thr, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 90
- (D) OTHER INFORMATION: /note= "Xaa at position 90 is Trp or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 91
- (D) OTHER INFORMATION: /note="Xaa at position 91 is Asn, Pro, Ala, Ser, Trp, Gln, Tyr, Leu, Lys, Ile, Asp, or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 92
- (D) OTHER INFORMATION: /note= "Xaa at position 92 is Glu or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 94

(C) OTHER INFORMATION: /note= "Xaa at position 94 is Arg,
Ala, or Ser"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 95
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,
Thr, Glu, Leu, or Ser"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 98
 (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr,
Val, or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 100
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Tyr
or Trp"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 101
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is Leu
or Ala"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 102
 (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys,
Thr, Val, Trp, Ser, Ala, His, Met, Phe, Tyr, or Ile"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 103
 (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr
or Ser"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 106
 (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,
Pro, Leu, His, Val, or Gln"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 107
 (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala,
Ser, Ile, Asn, Pro, Asp, or Gly"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 108
 (D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln,
Ser, Met, Trp, Arg, Phe, Pro, His, Ile, Tyr, or Cys"

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 109
 (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala,
Met, Glu, His, Ser, Pro, Tyr, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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Asn Cys Xaa Xaa Xaa Ile Xaa Glu Xaa Xaa Xaa Xaa Leu Lys Xaa Xaa
1           5           10           15

Xaa Xaa Xaa Xaa Xaa Asp Xaa Xaa Asn Leu Asn Xaa Glu Xaa Xaa Xaa
20           25           30

Ile Leu Met Xaa Xaa Asn Leu Xaa Xaa Xaa Asn Leu Glu Xaa Phe Xaa
35           40           45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Xaa Ile Glu Xaa Xaa Leu
50           55           60

Xaa Xaa Leu Xaa Xaa Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg
65           70           75           80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Asp Xaa Xaa Xaa Phe Xaa Xaa Lys
85           90           95

Leu Xaa Phe Xaa Xaa Xaa Xaa Leu Glu Xaa Xaa Xaa Xaa Gln Gln
100          105          110

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /note= "Xaa at position 3 is Ser, Gly, Asp, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn, His, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile, Ala, Leu, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site

- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr, His, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /note= "Xaa at position 12 is His or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln or Asn"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /note= "Xaa at position 16 is Pro or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu, Arg, Asn, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu, Val, Ser, Ala, Arg, Gln, Glu, Ile, Phe, Thr, or Met"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 21
- (D) OTHER INFORMATION: /note= "Xaa at position 21 is Leu, Ala, Asn, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 24
- (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 28
- (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly, Asp, Ser, Ala, Asn, Ile, Leu, Met, Tyr, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 31
- (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln, Val, Met, Leu, Ala, Asn, Glu, or Lys"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 32

(D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp,
Phe, Ser, Ala, Gln, Glu, His, Val, or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 36

(D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu,
Asn, Ser, or Asp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 37

(D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,
Arg, Pro, Thr, or His"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 41

(D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,
Leu, or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 42

(D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro,
Gly, Ser, Ala, Asn, Val, Leu, or Gln"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 48

(D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,
Pro, or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 50

(D) OTHER INFORMATION: /note= "Xaa at position 50 is Ala
or Asn"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 51

(D) OTHER INFORMATION: /note= "Xaa at position 51 is Val
or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 53

(D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser
or Phe"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 54

(D) OTHER INFORMATION: /note= "Xaa at position 54 is Leu
or Phe"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 55

(D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln,

Ala, Glu, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 62
- (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser, Val, Asn, Pro, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 63
- (D) OTHER INFORMATION: /note= "Xaa at position 63 is Ile or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 65
- (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys, Asn, Met, Arg, Ile, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 66
- (D) OTHER INFORMATION: /note= "Xaa at position 66 is Asn, Gly, Glu, or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 68
- (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu, Gln, Trp, Arg, Asp, Asn, Glu, His, Met, Phe, Ser, Thr, Tyr, or Val"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 73
- (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 74
- (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala or Trp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 77
- (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 79
- (D) OTHER INFORMATION: /note= "Xaa at position 79 is Thr, Asp, or Ala"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 81
- (D) OTHER INFORMATION: /note= "Xaa at position 81 is His,

Pro, Arg, Val, Gly, Asn, Ser, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 84
- (D) OTHER INFORMATION: /note= "Xaa at position 84 is His, Ile, Asn, Ala, Thr, Arg, Gln, Glu, Lys, Met, Ser, Tyr, Val, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 85
- (D) OTHER INFORMATION: /note= "Xaa at position 85 is Ile or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 86
- (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys or Arg"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 87
- (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp, Pro, Met, Lys, His, Pro, Asn, Ile, Leu, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 91
- (D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn, Pro, Ser, Ile, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 94
- (D) OTHER INFORMATION: /note= "Xaa at position 94 is Arg, Ala, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 95
- (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg, Thr, Glu, Leu, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 98
- (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 102
- (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys, Val, Trp, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 103
- (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr,

Ala, His, Phe, Tyr, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 106
- (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn, Pro, Leu, His, Val, or Gln"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 107
- (D) OTHER INFORMATION: /note= "Xaa at position 107 is Ala, Ser, Ile, Pro, or Asp"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 108
- (D) OTHER INFORMATION: /note= "Xaa at position 108 is Gln, Met, Trp, Phe, Pro, His, Ile, or Tyr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 109
- (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala, Met, Glu, Ser, or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Asn	Cys	Xaa	Xaa	Met	Ile	Asp	Glu	Xaa	Ile	Xaa	Xaa	Leu	Lys	Xaa	Xaa
1				5				10						15	
Pro	Xaa	Pro	Xaa	Xaa	Asp	Phe	Xaa	Asn	Leu	Asn	Xaa	Glu	Asp	Xaa	Xaa
			20					25					30		
Ile	Leu	Met	Xaa	Xaa	Asn	Leu	Arg	Xaa	Xaa	Asn	Leu	Glu	Ala	Phe	Xaa
		35					40					45			
Arg	Xaa	Xaa	Lys	Xaa	Xaa	Xaa	Asn	Ala	Ser	Ala	Ile	Glu	Xaa	Xaa	Leu
		50				55					60				
Xaa	Xaa	Leu	Xaa	Pro	Cys	Leu	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg
65				70				75						80	
Xaa	Pro	Ile	Xaa	Xaa	Xaa	Xaa	Gly	Asp	Trp	Xaa	Glu	Phe	Xaa	Xaa	Lys
			85					90						95	
Leu	Xaa	Phe	Tyr	Leu	Xaa	Xaa	Leu	Glu	Xaa	Xaa	Xaa	Xaa	Gln	Gln	
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AACAACCTCA ATGCTGAAGA CGTTGAT

27

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCAACGTCT TCAGCATT

18

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AACAACCTCA ATTCTGAAGA CATGGAT

27

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATCCATGTCT TCAGAATT

18

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CATGGGAACC ATATGTCAGG AT

22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATCCTGACAT ATGGTTCC

18

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TGAACCATAT GTCAGG

16

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AATTCCTGAC ATATGGTTCA TGCA

24

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AATTCGAACC ATATGTCAGA

20

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AGCTTCTGAC ATATGGTTTCG

20

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATCGAACCAT ATGTCAGATG CA

22

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TCTGACATAT GGTTCGAT

18

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCCTGATGG AACGAAACCT TCGACTTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

AAGTCGAAGG TTTCGTTCCA TCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATCCTGATGG AACGAAACCT TCGAACTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

AGTTCGAAGG TTTCGTTCCA TCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTCGCATTCG TAAGGGCTGT CAAG

24

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCTTACGAAT GCGAGCAGGT TTGG

24

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAGAGCTTCG TAAGGGCTGT CAAG

24

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCTTACGAAG CTCTCCAGGT TTGG

24

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CACTTAGAAA ATGCA

15

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TTTTCTAAGT GCTTGACAGC

20

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AACTTAGAAA ATGCA

15

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TTTCTAAGT TCTTGACAGC

20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGTGATTGGA TGTCGAGAGG GTGCGGCCGT GGCAGAGGGC AGACATGG

48

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA CCATCAAG

48

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GATGATTGGA TGTCGAGAGG GTGCGGCCGT GGCAGAGGGC AGACATGG

48

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCAAG

48

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TACGAGATTA CGAAGAAT

18

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CGTAATCTCG TACCATGT

18

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TTGGAGATTA CGAAGAAT

18

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGTAATCTCC AACCATGT

18

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TGCCTCAATA CCTGATGCA

19

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TCAGGTATTG AGGCAATTCT T

21

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

AATTCTTGCC AGTCACCTGC CTTGAT

26

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCAGGTGACT GGCAAG

16

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

AATTCCGGGA AAAACTGACG TTCTATCTGG TT

32

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CTCAAGGGAA ACCAGATAGA ACGTCAGTTT TTCCCGG

37

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCTTGAGC ACGCGCAGGA ACAACAGTAA TA

32

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGCTTATTAC TGTTGTTTCCT GCGCGTG

27

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACCCTTGAGC AAGCGCAGGA ACAACAGTAA TA

32

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

AGCTTATTAC TGTTGTTTCCT GCGCTTG

27

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1           5           10           15

Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
          20           25           30

Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
          35           40           45

Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
          50           55           60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65           70           75           80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
          85           90           95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
1           5           10           15

Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp Val Asp
          20           25           30

Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
          35           40           45

Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
          50           55           60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65           70           75           80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
          85           90           95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	1	5	10	15
Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp	20	25	30	
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	35	40	45	
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	50	55	60	
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	65	70	75	80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	85	90	95	
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln	100	105	110		

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Val	Pro	1	5	10	15
Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp	Met	Asp	20	25	30	
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn	35	40	45	
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile	Leu	50	55	60	
Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr	Arg	65	70	75	80
His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg	Lys	85	90	95	

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1 5 10 15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
20 25 30
Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala Phe Val
35 40 45
Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95
Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1 5 10 15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
20 25 30
Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val
35 40 45
Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu

Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp			
			20					25					30					
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn			
		35					40					45						
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu			
		50				55					60							
Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg			
		65			70					75					80			
His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Arg	Lys			
				85				90						95				
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln				
			100					105					110					

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln	Pro			
1				5				10						15				
Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln	Asp			
			20					25					30					
Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe	Asn			
		35					40					45						
Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu			
		50				55					60							
Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg			
		65			70					75					80			
His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Arg	Lys			
				85				90						95				
Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln				
			100					105					110					

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1 5 10 15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
20 25 30
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
35 40 45
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Glu Lys
85 90 95
Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1 5 10 15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
20 25 30
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
35 40 45
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Glu Lys
85 90 95
Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1           5           10           15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
          20           25           30
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
          35           40           45
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu
          50           55           60
Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
65           70           75           80
His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys
          85           90           95
Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
          100          105          110

```

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1           5           10           15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
          20           25           30
Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
          35           40           45
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu
          50           55           60
Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
65           70           75           80
His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys

```

Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
 100 105 110

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
 1 5 10 15
 Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
 20 25 30
 Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
 35 40 45
 Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala Ile Leu
 50 55 60
 Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg
 65 70 75 80
 His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys
 85 90 95
 Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln Gln
 100 105 110

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
 1 5 10 15
 Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp Val Asp
 20 25 30
 Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser Phe Val
 35 40 45

Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro
1 5 10 15

Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp
20 25 30

Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val
35 40 45

Arg Ala Val Lys His Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Val Pro
1 5 10 15

Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp Met Asp
20 25 30

Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala Phe Val
35 40 45

Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60

Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80

His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
1 5 10 15

Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp
20 25 30

Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
35 40 45

Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
1           5           10           15
Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp
          20           25           30
Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
          35           40           45
Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala
          50           55           60
Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80
Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
          100          105          110
Gln
```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
1           5           10           15
Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp
          20           25           30
Gln Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
          35           40           45
Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Gly Ile Glu Ala
          50           55           60
Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80
Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
```


	85	90	95
Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln			
	100	105	110
Gln			

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Ala	Ile	Glu	Ser
	50					55					60				
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Thr	Arg	His	Pro	Ile	His	Ile	Lys	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg
				85					90					95	
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Ala Ile Glu Ser
50 55 60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65 70 75 80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
85 90 95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Ala Ile Glu Ser
50 55 60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65 70 75 80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
85 90 95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
          20           25           30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35           40           45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50           55           60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100          105          110

Gln
  
```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
          20           25           30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35           40           45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50           55           60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80
  
```

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys

1	5	10	15
Arg Pro Pro Ala Pro Leu Leu Asp	Pro Asn Asn Leu Asn Ala Glu Asp		
20	25	30	
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser			
35	40	45	
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala			
50	55	60	
Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro			
65	70	75	80
Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg			
85	90	95	
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln			
100	105	110	
Gln			

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys			
1	5	10	15
Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp			
20	25	30	
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala			
35	40	45	
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala			
50	55	60	
Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro			
65	70	75	80
Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg			
85	90	95	
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln			
100	105	110	
Gln			

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
          20           25           30
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
          35           40           45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60
Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80
Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95
Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
          100          105          110
Gln
  
```

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15
Val Pro Pro Ala Pro Leu Leu Asp Ser Asn Asn Leu Asn Ser Glu Asp
          20           25           30
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Leu Ala
          35           40           45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60
  
```

Ile	Leu	Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Ser	Leu	Glu	His	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Val	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Thr	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
 20 25 30
 Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
 35 40 45
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Val Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Ser Leu Glu His Ala Gln Glu Gln
 100 105 110
 Gln

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAAGTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTTCCCTTGA GCACGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTTCCCTTGA GCACGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGGT TCCACCTGCA	60
CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGGT TCCACCTGCA	60
CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGGT TCCACCTGCA	60
CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTTCCCTTGA GCACGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGAGACCACC TGCACCTTTG	60
CTGGACCCGA ACAACCTCAA TGCTGAAGAC GTCGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCAGCGCA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGAGACCACC TAACCCTTTG	60
CTGGACCCGA ACAACCTCAA TTCTGAAGAC ATGGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGCAATT	180

GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCAGCGA 240
 CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT 300
 CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG 333

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGGTTCCACC TGCACCTTTG 60
 CTGGACAGTA ACAACCTCAA TTCCGAAGAC ATGGATATCC TGATGGAAAA TAACCTTCGT 120
 CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGCAATT 180
 GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCAGCGA 240
 CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT 300
 CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG 333

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG 60
 CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAACG AAACCTTCGA 120
 CTTCCAAACC TGCTCGCATT CGTAAGGGCT GTCAAGAACT TAGAAAATGC ATCAGCAATT 180
 GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCAGCGA 240
 CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT 300
 CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG 333

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAACG AAACCTTCGA	120
CTTCCAAACC TGGAGAGCTT CGTAAGGGCT GTCAAGAACT TAGAAAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAACG AAACCTTCGA	120
ACTCCAAACC TGCTCGCATT CGTAAGGGCT GTCAAGCACT TAGAAAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGGTATT	180
GAGGCAATTC TTCGTAATCT CCAACCATGT CTGCCCTCTG CCACGGCCGC ACCCTCTCGA	240
CATCCAATCA TCATCAAGGC AGGTGACTGG CAAGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGGTATT	180
GAGGCAATTC TTCGTAATCT CGTACCATGT CTGCCCTCTG CCACGGCCGC ACCCTCTCGA	240
CATCCAATCA CCATCAAGGC AGGTGACTGG CAAGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240

CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GGGAAAAACT GACGTTCTAT 300
CTGGTTACCC TTGAGCAAGC GCAGGAACAA CAG 333

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG 60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT 120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGCAATT 180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA 240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GGGAAAAACT GACGTTCTAT 300
CTGGTTTCCC TTGAGCACGC GCAGGAACAA CAG 333

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGAGACCACC TGCACCTTTG 60
CTGGACCCGA ACAACCTCAA TGCTGAAGAC GTCGATATCC TGATGGAACG AAACCTTCGA 120
CTTCCAAACC TGGAGAGCTT CGTAAGGGCT GTCAAGAACT TAGAAAATGC ATCAGCAATT 180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA 240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT 300
CTGAAACCT TGGAGAACGC GCAGGCTCAA CAG 333

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGAGACCACC TAACCCTTTG	60
CTGGACCCGA ACAACCTCAA TTCTGAAGAC ATGGATATCC TGATGGAACG AAACCTTCGA	120
ACTCCAAACC TGCTCGCATT CGTAAGGGCT GTCAAGCACT TAGAAAAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

AACTGCTCTA TAATGATCGA TGAAATTATA CATCACTTAA AGGTTCCACC TGCACCTTTG	60
CTGGACAGTA ACAACCTCAA TTCCGAAGAC ATGGATATCC TGATGGAACG AAACCTTCGA	120
CTTCCAAACC TGCTCGCATT CGTAAGGGCT GTCAAGAACT TAGAAAAATGC ATCAGCAATT	180
GAGAGCATTC TTAAAAATCT CCTGCCATGT CTGCCCCTGG CCACGGCCGC ACCCACGCGA	240
CATCCAATCC ATATCAAGGA CGGTGACTGG AATGAATTCC GTCGTAAACT GACCTTCTAT	300
CTGAAAACCT TGGAGAACGC GCAGGCTCAA CAG	333

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGGTATT	180
GAGGCAATTC TTCGTAATCT CCAACCATGT CTGCCCTCTG CCACGGCCGC ACCCTCTCGA	240
CATCCAATCA TCATCAAGGC AGGTGACTGG CAAGAATTCC GGGAAAAACT GACGTTCTAT	300
CTGGTTACCC TTGAGCAAGC GCAGGAACAA CAG	333

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGGTATT	180
GAGGCAATTC TTCGTAATCT CGTACCATGT CTGCCCTCTG CCACGGCCGC ACCCTCTCGA	240
CATCCAATCA CCATCAAGGC AGGTGACTGG CAAGAATTCC GGGAAAAACT GACGTTCTAT	300
CTGGTTACCC TTGAGCAAGC GCAGGAACAA CAG	333

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

AACTGCTCTA ACATGATCGA TGAAATCATC ACCCACCTGA AGCAGCCACC GCTGCCGCTG	60
CTGGACTTCA ACAACCTCAA TGGTGAAGAC CAAGATATCC TGATGGAAAA TAACCTTCGT	120
CGTCCAAACC TCGAGGCATT CAACCGTGCT GTCAAGTCTC TGCAGAATGC ATCAGGTATT	180
GAGGCAATTC TTCGTAATCT CGTACCATGT CTGCCCTCTG CCACGGCCGC ACCCTCTCGA	240

CATCCAATCA CCATCAAGGC AGGTGACTGG CAAGAATTCC GGGAAAACT GACGTTCTAT 300
CTGGTTTCCC TTGAGCACGC GCAGGAACAA CAG 333

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAAGTTAGA AAATGCATCA 180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC 240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCGTCG TAAACTGACC 300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAG 339

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120
CTTCGAACTC CAAACCTGCT CGCATTCTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC 240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCGTCG TAAACTGACC 300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAG 339

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGGT TCCACCTGCA	60
CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC	240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC	300
TTCTATCTGA AAACCTTGA GAACGCGCAG GCTCAACAG	339

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC	120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG 60
 CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC 120
 CTTGCTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA 180
 GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
 TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
 TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG 60
 CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAAAATAAC 120
 CTTGCTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA 180
 GGTATTGAGG CAATTCTTCG TAATCTCGTA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
 TCTCGACATC CAATCACCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
 TTCTATCTGG TTTCCCTTGA GCACGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Ala Pro Met Thr Gln Thr Thr Ser Leu Lys Thr Ser Trp Val Asn
 1 5 10 15
 Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro
 20 25 30
 Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile
 35 40 45
 Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg

50	55	60
Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu Lys		
65	70	75 80
Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg His		
	85	90 95
Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys Leu		
	100	105 110
Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln Thr Thr		
	115	120 125
Leu Ser Leu Ala Ile Phe		
130		

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /note= "Xaa at position 18 is Asn or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /note= "Xaa at position 19 is Met, Ala, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /note= "Xaa at position 20 is Ile, Pro, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 23
- (D) OTHER INFORMATION: /note= "Xaa at position 23 is Ile, Ala, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 25
- (D) OTHER INFORMATION: /note= "Xaa at position 25 is Thr or His"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 29
 (D) OTHER INFORMATION: /note= "Xaa at position 29 is Gln,
 Arg, Val, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 32
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Leu,
 Ala, Asn, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 34
 (D) OTHER INFORMATION: /note= "Xaa at position 34 is Leu
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 37
 (D) OTHER INFORMATION: /note= "Xaa at position 37 is Phe,
 Pro, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 38
 (D) OTHER INFORMATION: /note= "Xaa at position 38 is Asn
 or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 42
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Gly,
 Ala, Ser, Asp, or Asn"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 45
 (D) OTHER INFORMATION: /note= "Xaa at position 45 is Gln,
 Val, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 46
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Asp
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 49
 (D) OTHER INFORMATION: /note= "Xaa at position 49 is Met,
 Ile, Leu, or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 50
 (D) OTHER INFORMATION: /note= "Xaa at position 50 is Glu
 or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site

- (B) LOCATION: 51
- (D) OTHER INFORMATION: /note= "Xaa at position 51 is Asn, Arg, or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 55
- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Arg, Leu, or Thr"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 56
- (D) OTHER INFORMATION: /note= "Xaa at position 56 is Pro or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 59
- (D) OTHER INFORMATION: /note= "Xaa at position 59 is Glu or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 60
- (D) OTHER INFORMATION: /note= "Xaa at position 60 is Ala or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 62
- (D) OTHER INFORMATION: /note= "Xaa at position 62 is Asn Val, or Pro"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 63
- (D) OTHER INFORMATION: /note= "Xaa at position 63 is Arg or His"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 65
- (D) OTHER INFORMATION: /note= "Xaa at position 65 is Val or Ser"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 67
- (D) OTHER INFORMATION: /note= "Xaa at position 67 is Ser, Asn, His, or Gly"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 69
- (D) OTHER INFORMATION: /note= "Xaa at position 69 is Gln or Glu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 73

(D) OTHER INFORMATION: /note= "Xaa at position 73 is Ala
or Gly"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 76

(D) OTHER INFORMATION: /note= "Xaa at position 76 is Ser,
Ala, or Pro"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 79

(D) OTHER INFORMATION: /note= "Xaa at position 79 is Lys,
Arg, or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 82

(D) OTHER INFORMATION: /note= "Xaa at position 82 is Leu,
Glu, Val, or Trp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 85

(D) OTHER INFORMATION: /note= "Xaa at position 85 is Leu
or Val"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 87

(D) OTHER INFORMATION: /note= "Xaa at position 87 is Leu,
Ser, or Trp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 88

(D) OTHER INFORMATION: /note= "Xaa at position 88 is Ala
or Trp"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 91

(D) OTHER INFORMATION: /note= "Xaa at position 91 is Ala
or Pro"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 93

(D) OTHER INFORMATION: /note= "Xaa at position 93 is Pro
or Ser"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 95

(D) OTHER INFORMATION: /note= "Xaa at position 95 is His
or Thr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 98

(D) OTHER INFORMATION: /note= "Xaa at position 98 is His,
Ile, or Thr"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 100
 (D) OTHER INFORMATION: /note= "Xaa at position 100 is Lys
 or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 101
 (D) OTHER INFORMATION: /note= "Xaa at position 101 is Asp,
 Ala, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 105
 (D) OTHER INFORMATION: /note= "Xaa at position 105 is Asn
 or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 109
 (D) OTHER INFORMATION: /note= "Xaa at position 109 is Arg,
 Glu, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 112
 (D) OTHER INFORMATION: /note= "Xaa at position 112 is Thr
 or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 116
 (D) OTHER INFORMATION: /note= "Xaa at position 116 is Lys,
 Val, Trp, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 117
 (D) OTHER INFORMATION: /note= "Xaa at position 117 is Thr
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 120
 (D) OTHER INFORMATION: /note= "Xaa at position 120 is Asn,
 Gln, or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 123
 (D) OTHER INFORMATION: /note= "Xaa at position 123 is Ala
 or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Ala	Pro	Met	Thr	Gln	Thr	Thr	Ser	Leu	Lys	Thr	Ser	Trp	Val	Asn	Cys
1				5					10					15	

Ser Xaa Xaa Xaa Asp Glu Xaa Ile Xaa His Leu Lys Xaa Pro Pro Xaa

20	25	30
Pro Xaa Leu Asp Xaa Xaa Asn Leu Asn Xaa Glu Asp Xaa Xaa Ile Leu		
35	40	45
Xaa Xaa Xaa Asn Leu Arg Xaa Xaa Asn Leu Xaa Xaa Phe Xaa Xaa Ala		
50	55	60
Xaa Lys Xaa Leu Xaa Asn Ala Ser Xaa Ile Glu Xaa Ile Leu Xaa Asn		
65	70	75
Leu Xaa Pro Cys Xaa Pro Xaa Xaa Thr Ala Xaa Pro Xaa Arg Xaa Pro		
85	90	95
Ile Xaa Ile Xaa Xaa Gly Asp Trp Xaa Glu Phe Arg Xaa Lys Leu Xaa		
100	105	110
Phe Tyr Leu Xaa Xaa Leu Glu Xaa Ala Gln Xaa Gln Gln Thr Thr Leu		
115	120	125
Ser Leu Ala Ile Phe		
130		

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "Met- or Met-Ala may or may not precede the amino acid in position 1"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 4
- (D) OTHER INFORMATION: /note= "Xaa at position 4 is Asn or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /note= "Xaa at position 5 is Met, Ala, or Ile"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /note= "Xaa at position 6 is Ile, Pro, or Leu"

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "Xaa at position 9 is Ile,

Ala, or Leu"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 11
 (D) OTHER INFORMATION: /note= "Xaa at position 11 is Thr
 or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 15
 (D) OTHER INFORMATION: /note= "Xaa at position 15 is Gln,
 Arg, Val, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 18
 (D) OTHER INFORMATION: /note= "Xaa at position 18 is Leu,
 Ala, Asn, or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 20
 (D) OTHER INFORMATION: /note= "Xaa at position 20 is Leu
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 23
 (D) OTHER INFORMATION: /note= "Xaa at position 23 is Phe,
 Pro, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 24
 (D) OTHER INFORMATION: /note= "Xaa at position 24 is Asn
 or Ala"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 28
 (D) OTHER INFORMATION: /note= "Xaa at position 28 is Gly,
 Ala, Ser, Asp, or Asn"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 31
 (D) OTHER INFORMATION: /note= "Xaa at position 31 is Gln,
 Val, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 32
 (D) OTHER INFORMATION: /note= "Xaa at position 32 is Asp
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 35
 (D) OTHER INFORMATION: /note= "Xaa at position 35 is Met,
 Ile, Leu, or Asp"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 36
 (D) OTHER INFORMATION: /note= "Xaa at position 36 is Glu
 or Asp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 37
 (D) OTHER INFORMATION: /note= "Xaa at position 37 is Asn,
 Arg, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 41
 (D) OTHER INFORMATION: /note= "Xaa at position 41 is Arg,
 Leu, or Thr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 42
 (D) OTHER INFORMATION: /note= "Xaa at position 42 is Pro
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 45
 (D) OTHER INFORMATION: /note= "Xaa at position 45 is Glu
 or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 46
 (D) OTHER INFORMATION: /note= "Xaa at position 46 is Ala
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 48
 (D) OTHER INFORMATION: /note= "Xaa at position 48 is Asn,
 Val, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 49
 (D) OTHER INFORMATION: /note= "Xaa at position 49 is Arg
 or His"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 51
 (D) OTHER INFORMATION: /note= "Xaa at position 51 is Val
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 53
 (D) OTHER INFORMATION: /note= "Xaa at position 53 is Ser,
 Asn, His, or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 55

- (D) OTHER INFORMATION: /note= "Xaa at position 55 is Gln
or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 59
 (D) OTHER INFORMATION: /note= "Xaa at position 59 is Ala
or Gly"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 62
 (D) OTHER INFORMATION: /note= "Xaa at position 62 is Ser,
Ala, or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 65
 (D) OTHER INFORMATION: /note= "Xaa at position 65 is Lys,
Arg, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 67
 (D) OTHER INFORMATION: /note= "Xaa at position 67 is Leu,
Glu, or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 68
 (D) OTHER INFORMATION: /note= "Xaa at position 68 is Leu,
Glu, Val, or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 71
 (D) OTHER INFORMATION: /note= "Xaa at position 71 is Leu
or Val"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 73
 (D) OTHER INFORMATION: /note= "Xaa at position 73 is Leu,
Ser, or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 74
 (D) OTHER INFORMATION: /note= "Xaa at position 74 is Ala
or Trp"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 77
 (D) OTHER INFORMATION: /note= "Xaa at position 77 is Ala
or Pro"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 79
 (D) OTHER INFORMATION: /note= "Xaa at position 79 is Pro"

or Ser"

- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 81
 (D) OTHER INFORMATION: /note= "Xaa at position 81 is His
 or Thr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 84
 (D) OTHER INFORMATION: /note= "Xaa at position 84 is His,
 Ile, or Thr"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 86
 (D) OTHER INFORMATION: /note= "Xaa at position 86 is Lys
 or Arg"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 87
 (D) OTHER INFORMATION: /note= "Xaa at position 87 is Asp,
 Ala, or Met"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 91
 (D) OTHER INFORMATION: /note= "Xaa at position 91 is Asn
 or Glu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 95
 (D) OTHER INFORMATION: /note= "Xaa at position 95 is Arg,
 Glu, or Leu"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 98
 (D) OTHER INFORMATION: /note= "Xaa at position 98 is Thr
 or Gln"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 102
 (D) OTHER INFORMATION: /note= "Xaa at position 102 is Lys,
 Val, Trp, or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 103
 (D) OTHER INFORMATION: /note= "Xaa at position 103 is Thr
 or Ser"
- (ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 106
 (D) OTHER INFORMATION: /note= "Xaa at position 106 is Asn,
 Gln, or His"
- (ix) FEATURE:

(A) NAME/KEY: Modified-site
 (B) LOCATION: 109
 (D) OTHER INFORMATION: /note= "Xaa at position 109 is Ala
 or Glu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asn	Cys	Ser	Xaa	Xaa	Xaa	Asp	Glu	Xaa	Ile	Xaa	His	Leu	Lys	Xaa	Pro
1				5					10					15	
Pro	Xaa	Pro	Xaa	Leu	Asp	Xaa	Xaa	Asn	Leu	Asn	Xaa	Glu	Asp	Xaa	Xaa
			20					25					30		
Ile	Leu	Xaa	Xaa	Xaa	Asn	Leu	Arg	Xaa	Xaa	Asn	Leu	Xaa	Xaa	Phe	Xaa
		35				40					45				
Xaa	Ala	Xaa	Lys	Xaa	Leu	Xaa	Asn	Ala	Ser	Xaa	Ile	Glu	Xaa	Ile	Leu
	50					55					60				
Xaa	Asn	Xaa	Xaa	Pro	Cys	Xaa	Pro	Xaa	Xaa	Thr	Ala	Xaa	Pro	Xaa	Arg
65					70					75					80
Xaa	Pro	Ile	Xaa	Ile	Xaa	Xaa	Gly	Asp	Trp	Xaa	Glu	Phe	Arg	Xaa	Lys
			85						90					95	
Leu	Xaa	Phe	Tyr	Leu	Xaa	Xaa	Leu	Glu	Xaa	Ala	Gln	Xaa	Gln	Gln	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTAGCCACGG CCGCACCCAC GCGACATCCA ATCCATATCA AGGACGGTGA CTGGAATG 58

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TTAACATTCC AGTCACCGTC CTTGATATGG ATTGGATGTC GCGTGGGTGC GGCCGTGG 58

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

AAGGAGATAT ATCCATGAAC TGCTCTAAC

29

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Asn Cys Ser Asn
1 5

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln
1 5 10 15
Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln
20 25 30
Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe
35 40 45
Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile
50 55 60
Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr
65 70 75 80
Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg

Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
 100 105 110

Thr Thr Leu Arg Leu Ala Ile Phe
 115 120

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

AATTCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGA 60
 CCACTCTGTC G 71

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

CTAGCGACAG AGTGGTCTGT TGAGCCTGCG CGTTCTCCAA GGTTTTCAGA TAGAAGGTCA 60
 GTTTACGACG G 71

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Met Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln
 1 5 10 15

Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln

	20		25		30										
Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe
	35						40					45			
Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile
	50					55					60				
Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	Thr
	65				70					75				80	
Arg	His	Pro	Ile	His	Ile	Lys	Ala	Gly	Asp	Trp	Asn	Glu	Phe	Arg	Arg
			85					90					95		
Lys	Leu	Thr	Phe	Tyr	Leu	Lys	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	Gln
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Met	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	Gln
1				5				10						15	
Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Gly	Glu	Asp	Gln
			20					25					30		
Asp	Ile	Leu	Met	Glu	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	Phe
			35				40					45			
Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	Ile
	50					55					60				
Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala					
	65				70				75						

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

CTAGCCACGG CCGCACCCAC GCGACATCCA ATCCATATCA AGGCTGGTGA CTGGAATG

58

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AATTCATTCC AGTCACCAGC CTTGATATGG ATTGGATGTC GCGTGGGTGC GGCCGTGG

58

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

AATTCGTCG TAAACTGACC TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAGT

60

AATA

64

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCTTATTAC TGTGAGCCT GCGCGTTCTC CAAGGTTTTT AGATAGAAGG TCAGTTTACG

60

ACGG

64

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 408 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ATGGCTCCAA TGACTCAGAC TACTTCTCTT AAGACTTCTT GGGTAACTG CTCTAACATG	60
ATCGATGAAA TTATAACACA CTAAAGCAG CCACCTTTGC CTTTGCTGGA CTTCAACAAC	120
CTCAATGGGG AAGACCAAGA CATTCTGATG GAAAATAACC TTCGAAGGCC AAACCTGGAG	180
GCATTCAACA GGGCTGTCAA GAGTTTACAG AATGCATCAG CAATTGAGAG CATTCTTAAA	240
AATCTCCTGC CATGTCTGCC CCTGGCCACG GCCGCACCCA CGCGACATCC AATCCATATC	300
AAGGACGGTG ACTGGAATGA ATTCCGTCGT AAACCTGACCT TCTATCTGAA AACCTTGGAG	360
AACGCGCAGG CTCAACAGAC CACTCTGTCT CTAGCGATCT TTTAATAA	408

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ATC GAT GAA ATC ATC ACC CAC CTG AAG CAG CCA CCG CTG CCG CTG CTG	48
Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu Pro Leu Leu	
1 5 10 15	
GAC TTC AAC AAC CTC AAT GGT GAA GAC CAA GAT ATC CTG ATG GAA AAT	96
Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu Met Glu Asn	
20 25 30	
AAC CTT CGT CGT CCA AAC CTC GAG GCA TTC AAC CGT GCT GTC AAG TCT	144
Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala Val Lys Ser	
35 40 45	
CTG CAG AAT GCA T	157
Leu Gln Asn Ala	
50	

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro Pro Leu Pro Leu Leu
1 5 10 15
Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp Ile Leu Met Glu Asn
20 25 30
Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn Arg Ala Val Lys Ser
35 40 45
Leu Gln Asn Ala
50

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCATGGCTCC AATGACTCAG ACTACTTCTC TTAAGACTTC TTGGGTAAAC TGCTCTAACA 60
TGATCGATGA AATTATAACA CACTTAAAGC AGCCACCTTT GCCTTTGCTG GACTTCAACA 120
ACCTCAATGG GGAAGACCAA GACATTCTGA TGGAAAATAA CCTTCGAAGG CCAAACCTGG 180
AGGCATTCAA CAGGGCTGTC AAGAGTTTAC AGAATGCATC AGCAATTGAG AGCATTCTTA 240
AAAATCTCCT GCCATGTCTG CCCCTGGCCA CGGCCGCACC CACGCGACAT CCAATCCATA 300
TCAAGGACGG TGA CTGGAAT GAATTCCGTC GTAACTGAC CTTCTATCTG AAAACCTTGG 360
AGAACGCGCA GGCTCAACAG ACCACTCTGT CGCTAGCGAT CTTTAAATAA GCTT 414

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

AAGCTTATTA AAAGATCGCT AGCGACAGAG TGGTCTGTTG AGCCTGCGCG TTCTCCAAGG 60

TTTTCAGATA GAAGGTCAGT TTACGACGGA ATTCATTCCA GTCACCGTCC TTGATATGGA 120
 TTGGATGTCG CGTGGGTGCG GCCGTGGCCA GGGGCAGACA TGGCAGGAGA TTTTAAAGAA 180
 TGCTCTCAAT TGCTGATGCA TTCTGTAAAC TCTTGACAGC CCTGTTGAAT GCCTCCAGGT 240
 TTGGCCTTCG AAGGTTATTT TCCATCAGAA TGTCTTGGTC TTCCCCATTG AGGTTGTTGA 300
 AGTCCAGCAA AGGCAAAGGT GGCTGCTTTA AGTGTGTTAT AATTTTCATCG ATCATGTTAG 360
 AGCAGTTAAC CCAAGAAGTC TTAAGAGAAG TAGTCTGAGT CATTGGAGCC ATGG 414

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ATGATGATTA CTCTGCGCAA ACTTCCTCTG GCGGTTGCCG TCGCAGCGGG CGTAATGTCT 60
 GCTCAGGCCA TGGCTAACTG C 81

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GCAGTTAGCC ATGGCCTGAG CAGACATTAC GCCCGCTGCG ACGGCAACCG CCAGAGGAAG 60
 TTTGCGCAGA GTAATCATCA T 81

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

CATGGCTAAC TGCTCTAACA TGAT

24

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CGATCATGTT AGAGCAGTTA GC

22

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ATGGCTAACT GC

12

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Met Ala Asn Cys
1

(2) INFORMATION FOR SEQ ID NO:155:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GCCGATACCG CGGCATACTC CCACCATTCA GAGA

34

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GCCGATAAGA TCTAAAACGG GTATGGAGAA ACA

33

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATAGTCTTCC CCAGATATCT AACGCTTGAG

30

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CAATACCTGA TGC GTTTTCT AAGT

24

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GGTTTCGTTC CATCAGAATG TCCATGTCTT CAG

33

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ATATCCTGAT GGAACGAAAC 120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAACGCATCA 180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG 300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60

CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACATGG ACATTTGATG GAACGAAACC 120

TTCGAACTCC AAACCTGCTC GCATTCGTAA GGGCTGTCAA GCACTTAGAA AACGCATCAG 180

GTATTGAGGC AATTCCTTCGT AATCTCCAAC CATGTCTGCC CTCTGCCACG GCCGCACCCT 240

CTCGACATCC AATCATCATC AAGGCAGGTG ACTGGCAAGA ATTCGGGGA AAACTGACGT 300

TCTATCTGGT TACCCTTGAG CAAGCGCAGG AACAACAG 338

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CATGGCTAAC TGCTCTAACA TGATCGATGA AATTATAACA

40

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CTTTAAGTGT GTTATAATTT CATCGATCAT GTTAGAGCAG TTAGC

45

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CACTTAAAGC AGCCACCTTT GCCTTTGCTG GACTTC

36

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAGGTTGTTG AAGTCCAGCA AAGGCAAAGG TGGCTG

36

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

AACAACCTCA ATGACGAAGA CATGTCT

27

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

AGACATGTCT TCGTCATT

18

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

TGAACCATAT GTCAGG

16

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

AATTCCTGAC ATATGGTTCA TGCA

24

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

CATGGCAAAC TGCTCTATAG CTATCGATGA AATTATACAT

40

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

CTTTAAGTGA TGTATAATTT CATCGATAGC TATAGAGCAG TTTGC

45

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CATGGCAAAC TGCTCTATAA TCATCGATGA AATTATACAT

40

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

CTTTAAGTGA TGTATAATTT CATCGATGAT TATAGAGCAG TTTGC

45

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

ATCCTGGACG AACGAAACCT TCGAACTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

AGTTCGAAGG TTTCGTTCGT CCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

ATCCTGATCG AACGAAACCT TCGAACTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

AGTTCGAAGG TTTCGTTCTGA TCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATCCTGCTGG AACGAAACCT TCGAACTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

AGTTCGAAGG TTTCGTTCCA GCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

AACAACCTCA ATTCTGAAGA CGTTGAT

27

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

ATCAACGTCT TCAGAATT

18

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

CGCGCCATGG CTAAGTCTC TATAATGATC GATGAAGCAA TACATCACTT A

51

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGCGTCGATA AGCTTATT

18

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GGAGATATAT CCATGGCT

18

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TCGGTCCATC AGAATAGACA TGTCTTCAGC ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

TCGGTCCATC AGAATAGAAA CGTCTTCAGC ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

TCGGTCCATC AGAATAGACA TGTCTTCGTC ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

TCGGTCCATC AGAATAGAAA CGTCTTCGTC ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TCGGTCCATC AGAATAGACA TGTCTTCAGA ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCGGTCCATC AGAATAGAAA CGTCTTCAGA ATTGAGGTTG TT

42

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGCCCTCTG CCACGGCCGC ACCCTCTCGA CATCCAATCA TCATCCGT

48

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

AATTCTTGCC AGTCACCTGC ACGGAT

26

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATGGGTGACT GGCAAG

16

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

AATTCTTGCC AGTCACCCAT ACGGAT

26

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CATGGCTAAC TGCTCTATTA TGATCGATGA AGCAATACAT

40

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

CTTTAAGTGA TGTATTGCTT CATCGATCAT AATAGAGCAG TTAGC

45

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

CACTTAAAGG TACCACCTCG CCCTTCCCTG GACCCG

36

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GAGGTTGTTT GGGTCCAGG AAGGGCGAGG TGGTAC

36

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

CACTTAAAGA GACCACCTGC ACCTTCCCTG GACCCG

36

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GAGGTTGTTC GGGTCCAGGG AAGGTGCAGG TGGTCT

36

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

AACAACCTCA ATGACGAAGA CATGGAT

27

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

ATCCATGTCT TCGTCATT

18

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

AACAACCTCA ATGACGAAGA CGTCGAT

27

(2) INFORMATION FOR SEQ ID NO:204:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

ATCGACGTCT TCGTCATT

18

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

AACAACCTCA ATGACGAAGA CATGTCT

27

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

AGACATGTCT TCGTCATT

18

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

AACAACCTCA ATGACGAAGA CGTCTCT

27

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGAGACGTCT TCGTCATT

18

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

ATCCTGATGG ACCGAAACCT TCGACTTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

AAGTCGAAGG TTTCGGTCCA TCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ATCCTGATGG ACCGAAACCT TCGACTTAGC AACCTG

36

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CCTTACGAAG CTCTCCAGGT TGCT

24

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

CGTAATCTCT GGCCATGT

18

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

CCAGAGATTA CGAAGAAT

18

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

AATTCCGGGA AAAACTGCAA TTCTATCTGT GG

32

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTCAAGGGTC CACAGATAGA ATTGCAGTTT TTCCCGG

37

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

AATTCCGGGA AAAACTGCAA TTCTATCTGG TT

32

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

CTCAAGGGTA ACCAGATAGA ATTGCAGTTT TTCCCGG

37

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

AATTCCGGGA AAAACTGACG TTC

23

(2) INFORMATION FOR SEQ ID NO:220:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

AACCAGATAG AACGTCAGTT TTTCCCGG

28

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

TATCTGGTTA CCCTTGAGTA ATA

23

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGCTTATTAC TTCAAGGGT

19

(2) INFORMATION FOR SEQ ID NO:223:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AATTCCGGGA AAAACTGCAA TTC

23

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

AACCAGATAG AATTGCAGTT TTTCCCGG

28

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

CGATCATTAT AGAGCAGTTA GCCTTGTCAT CGTCGTCCTT GTAATCAGTT TCTGGATATG

60

C

61

(2) INFORMATION FOR SEQ ID NO:226:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

CATGGCATAT CCAGAACTG ATTACAAGGA CGACGATGAC AAGGCTAACT GCTCTATAAT 60

GAT 63

(2) INFORMATION FOR SEQ ID NO:227:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

AATTCCGGCT TAAACTGCAA TTCTATCTGT CT 32

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

CTCAAGGGTA GACAGATAGA ATTGCAGTTT AAGCCGG 37

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

TCTCTTGAGC AAGCGCAGGA ACAACAGTAA TA 32

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

CATGGCAAAC TGCTCTATAA TACTCGATGA AGCAATACAT

40

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CTTTAAGTGA TGTATTGCTT CATCGAGTAT TATAGAGCAG TTTGC

45

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

CATGGCAAAC TGCTCTATAA TGCCAGATGA AGCAATACAT

40

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

CTTTAAGTGA TGTATTGCTT CATCTGGCAT TATAGAGCAG TTTGC

45

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

CATGGCAAAC TGCTCTATAA TGATCGATGA AACTGATACA T

41

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

CTTTAAGTGA TGTATCAGTT CATCGATCAT TATAGAGCAG TTTGC

45

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

CACTTAAAGA TACCACCTAA CCCTAGCCTG GACAGT

36

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GAGGTTAGCA CTGTCCAGGC TAGGGTTAGG TGGTAT

36

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GCTAACCTCA ATTCCGAAGA CGTCTCT

27

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

AGAGACGTCT TCGGAATT

18

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

ATCCTGATGG ACTCCAACCT TCGAACTCCA AACCTG

36

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

AGTTCGAAGG TTGGAGTCCA TCAGGAT

27

(2) INFORMATION FOR SEQ ID NO:242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GTTCCCTATT GGACGGCCCC TCCCTCTCGA ACACCAATCA CGATCAAG

48

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

CGTGATTGGT GTTCGAGAGG GAGGGGCCGT CCAATAGGGA ACACATGG

48

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

CTCGATTCC CACATGCTTC TAAG

24

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

CTCGCATTCC CACATGCTGT CAAG

24

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

ATGTGGAAT GCGAGCAGGT TTGG

24

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

TTTCTAATT GCTTAGAAGC

20

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

CAATTAGAAA ATGCA

15

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

TTTTCTAATT GCTTGACAGC

20

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

TCAGGTATTG AGCCAATTCT T

21

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

TGGCTCAATA CCTGATGCA

19

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

TCTAATCTCC AACCATGT

18

(2) INFORMATION FOR SEQ ID NO:253:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

TTGGAGATTA GAAAGAAT

18

(2) INFORMATION FOR SEQ ID NO:254:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CTCAAGAGAA GACAGATAGA ATTGCAGTTT AAGCCGG

37

(2) INFORMATION FOR SEQ ID NO:255:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 40 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

CATGGCTAAC TGCTCTATAA TGATCGATGA AATTATACAT

40

(2) INFORMATION FOR SEQ ID NO:256:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

AATCCGGCT TAAACTGCAA TTCTATCTGT CTACCCTTTA ATA

43

(2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

AGCTTATTAA AGGGTAGACA GATAGAATTG CAGTTTAAGC CGG

43

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

AATTCGGCT TAAACTGCAA TTCTATCTGT CTACCCTTTA ATA

43

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
1 5 10 15

Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Asp Glu Asp
20 25 30

Met Ser Ile Leu Met Asp Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
35 40 45

Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser
50 55 60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65 70 75 80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
85 90 95

Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
1 5 10 15
Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Asp Glu Asp
20 25 30
Met Ser Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
35 40 45
Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser
50 55 60
Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65 70 75 80
Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
85 90 95
Arg Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
1 5 10 15

Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Asp Glu Asp
20 25 30

Met Ser Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
35 40 45

Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser
50 55 60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65 70 75 80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
85 90 95

Arg Lys Leu Thr Phe Tyr Leu Trp Thr Leu Glu Asn Ala Gln Ala Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
1 5 10 15

Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Asp Glu Asp
20 25 30

Met Ser Ile Leu Met Asp Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
35 40 45

Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser
50 55 60

Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65 70 75 80

Thr Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg
85 90 95

Arg Lys Leu Thr Phe Tyr Leu Trp Thr Leu Glu Asn Ala Gln Ala Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Met	Ala	Asn	Cys	Ser	Asn	Met	Ile	Asp	Glu	Ile	Ile	Thr	His	Leu	Lys	1	5	10	15
Gln	Pro	Pro	Leu	Pro	Leu	Leu	Asp	Phe	Asn	Asn	Leu	Asn	Asp	Glu	Asp	20	25	30	
Met	Ser	Ile	Leu	Met	Asp	Asn	Asn	Leu	Arg	Arg	Pro	Asn	Leu	Glu	Ala	35	40	45	
Phe	Asn	Arg	Ala	Val	Lys	Ser	Leu	Gln	Asn	Ala	Ser	Ala	Ile	Glu	Ser	50	55	60	
Ile	Leu	Lys	Asn	Leu	Leu	Pro	Cys	Leu	Pro	Leu	Ala	Thr	Ala	Ala	Pro	65	70	75	80
Thr	Arg	Arg	Pro	Ile	Ile	Ile	Arg	Asp	Gly	Asp	Trp	Asn	Glu	Phe	Arg	85	90	95	
Arg	Lys	Leu	Thr	Phe	Tyr	Leu	Trp	Thr	Leu	Glu	Asn	Ala	Gln	Ala	Gln	100	105	110	
Gln																			

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met	Ala	Asn	Cys	Ser	Ile	Ala	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	1	5	10	15
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp	20	25	30	
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala	35	40	45	
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	50	55	60	
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro				

65		70		75		80									
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Met	Ala	Asn	Cys	Ser	Ile	Ile	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
			35				40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70					75					80	
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30
 Val Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Met Ala Asn Cys Ser Ile Ala Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30
 Val Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Met Ala Asn Cys Ser Ile Ile Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30
Met Asp Ile Leu Ile Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Leu Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:271:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30
Met Asp Ile Leu Asp Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:272:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Met Ala Asn Cys Ser Ile Ala Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30
Val Asp Ile Leu Ile Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Met Ala Asn Cys Ser Ile Ile Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30
Val Asp Ile Leu Ile Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Ala Asn Cys Ser Ile Ala Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30
Val Asp Ile Leu Leu Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Met Ala Asn Cys Ser Ile Ile Ile Asp Glu Ile Ile His His Leu Lys
 1 5 10 15
 Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
 20 25 30
 Val Asp Ile Leu Leu Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Met Ala Asn Cys Ser Ile Ala Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30
Val Asp Ile Leu Asp Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:277:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met Ala Asn Cys Ser Ile Ile Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30
Val Asp Ile Leu Asp Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:278:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5				10						15	
Val	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20				25						30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala
			35				40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
			50				55					60			
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70					75						80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:279:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5				10						15	
Val	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Ser	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20				25						30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Leu	Ala

	35		40		45										
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
50						55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Gln	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Val	Ser	Ile	Leu	Met	Asp	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
			35				40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
50					55					60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asn Glu Asp
20 25 30
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30

Met Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Met Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30
Met Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg

85

90

95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
100 105

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Met Asp Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Gln Phe Tyr Leu Val Thr Leu Glu
100 105

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Gln Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln

(2) INFORMATION FOR SEQ ID NO:290:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Met Asp Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
 1 5 10 15
 Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
 20 25 30
 Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
 35 40 45
 Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu
 100 105

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Gln Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Val Pro Pro Arg Pro Ser Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Trp Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
50						55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Gln	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Ala	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp
			20					25					30		
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
		35					40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
50					55					60					
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Gln	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30
Val Asp Ile Leu Met Asp Arg Asn Leu Arg Leu Ser Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:297:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Ser Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
 20 25 30
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
 35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
 20 25 30
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser

	35		40		45										
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ala	Ile	His	His	Leu	Lys
1				5				10						15	
Arg	Pro	Pro	Ala	Pro	Ser	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Asp	Glu	Asp
			20					25					30		
Met	Ser	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
			35				40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		

Gln

(2) INFORMATION FOR SEQ ID NO:301:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
 1           5           10           15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
      20           25           30

Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
      35           40           45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
      50           55           60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
      85           90           95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
      100          105          110

Gln
```

(2) INFORMATION FOR SEQ ID NO:302:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```
Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
 1           5           10           15

Val Pro Pro Arg Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
      20           25           30

Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
      35           40           45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
      50           55           60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
      85           90           95
```

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Arg Met Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Trp Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Arg Met Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
1 5 10 15
Val Pro Pro Arg Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30
Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30
Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg

85

90

95

Glu Lys Leu Gln Phe Tyr Leu Val Thr Leu Glu
100 105

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30

Val Asp Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Val Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:310:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30

Met Ser Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:311:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30
Val Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Ser Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:312:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
1 5 10 15
Arg Pro Pro Ala Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
20 25 30
Met Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45
Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp
20 25 30

Val Asp Ile Leu Met Glu Arg Asn Leu Arg Leu Pro Asn Leu Glu Ser
35 40 45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Glu Lys Leu Gln Phe Tyr Leu Trp Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:314:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Met Asp Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Ala Pro Leu Leu Asp Pro Asn Asn Leu Asn Ala Glu Asp

	20		25		30										
Val	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser
	35						40					45			
Phe	Val	Arg	Ala	Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50				55						60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65					70					75					80
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
			85						90					95	
Glu	Lys	Leu	Thr	Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Met	Ala	Tyr	Pro	Glu	Thr	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys	Asn	Cys
1				5				10						15	
Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys	Arg	Pro	Pro	Ala
			20					25					30		
Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ala	Glu	Asp	Val	Asp	Ile	Leu
			35				40					45			
Met	Glu	Arg	Asn	Leu	Arg	Leu	Pro	Asn	Leu	Glu	Ser	Phe	Val	Arg	Ala
	50					55					60				
Val	Lys	Asn	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala	Ile	Leu	Arg	Asn
65					70					75					80
Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro	Ser	Arg	His	Pro
			85					90						95	
Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg	Glu	Lys	Leu	Thr
			100					105					110		
Phe	Tyr	Leu	Val	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln	Gln			
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Met Ala Tyr Pro Glu Thr Asp Tyr Lys Asp Asp Asp Asp Lys Asn Cys
1 5 10 15
Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys Arg Pro Pro Asn
20 25 30
Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp Met Asp Ile Leu
35 40 45
Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala Phe Val Arg Ala
50 55 60
Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala Ile Leu Arg Asn
65 70 75 80
Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro Ser Arg His Pro
85 90 95
Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg Glu Lys Leu Thr
100 105 110
Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln Gln
115 120 125

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Met Ala Asn Cys Ser Ile Met Pro Asp Glu Ala Ile His His Leu Lys
1 5 10 15
Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp
20 25 30
Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:318:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Leu Ile His His Leu Lys
1 5 10 15
Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp
20 25 30
Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:319:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
1 5 10 15

Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp
20 25 30
Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Pro
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg Thr Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Met Ala Asn Cys Ser Ile Ile Leu Asp Glu Ala Ile His His Leu Lys
1 5 10 15
Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp
20 25 30
Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Pro
50 55 60
Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80
Ser Arg Thr Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
          20           25           30

Met Asp Ile Leu Met Asp Ser Asn Leu Arg Thr Pro Asn Leu Leu Ala
          35           40           45

Phe Pro His Ala Ser Lys Gln Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
          65           70           75           80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
          100          105          110

Gln
  
```

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
          20           25           30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
          35           40           45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
  
```

65		70		75		80									
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Leu	Lys	Leu	Gln	Phe	Tyr	Leu	Ser	Thr	Leu	Glu	Gln	Ala	Gln	Glu	Gln
			100					105					110		
Gln															

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	
Arg	Pro	Pro	Asn	Pro	Leu	Leu	Asp	Pro	Asn	Asn	Leu	Asn	Ser	Glu	Asp
			20					25					30		
Met	Asp	Ile	Leu	Met	Glu	Arg	Asn	Leu	Arg	Thr	Pro	Asn	Leu	Leu	Ala
			35				40					45			
Phe	Val	Arg	Ala	Val	Lys	His	Leu	Glu	Asn	Ala	Ser	Gly	Ile	Glu	Ala
	50					55					60				
Ile	Leu	Arg	Asn	Leu	Gln	Pro	Cys	Leu	Pro	Ser	Ala	Thr	Ala	Ala	Pro
65				70					75					80	
Ser	Arg	His	Pro	Ile	Ile	Ile	Lys	Ala	Gly	Asp	Trp	Gln	Glu	Phe	Arg
				85					90					95	
Leu	Lys	Leu	Gln	Phe	Tyr	Leu	Ser	Thr	Leu						
			100					105							

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Met	Ala	Asn	Cys	Ser	Ile	Met	Ile	Asp	Glu	Ile	Ile	His	His	Leu	Lys
1				5					10					15	

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Leu Lys Leu Gln Phe Tyr Leu Ser Ser Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1 5 10 15

Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
20 25 30

Met Asp Ile Leu Met Asp Ser Asn Leu Leu Thr Pro Asn Leu Leu Ala
35 40 45

Phe Pro His Ala Ser Lys Gln Leu Glu Asn Ala Ser Gly Ile Glu Ala
50 55 60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65 70 75 80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Leu Lys Leu Gln Phe Tyr Leu Ser Ser Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
          20           25           30
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
          35           40           45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Pro
          50           55           60
Ile Leu Ser Asn Leu Gln Pro Cys Val Pro Tyr Trp Thr Ala Pro Pro
65           70           75           80
Ser Arg Thr Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95
Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
          100          105          110
Gln
  
```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ile Ile His His Leu Lys
1           5           10           15
Arg Pro Pro Asn Pro Leu Leu Asp Pro Asn Asn Leu Asn Ser Glu Asp
          20           25           30
Met Asp Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
          35           40           45
Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Pro
          50           55           60
Ile Leu Ser Asn Leu Gln Pro Cys Val Pro Tyr Trp Thr Ala Pro Pro
65           70           75           80
  
```

Ser Arg Thr Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Leu Lys Leu Gln Phe Tyr Leu Ser Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Leu Ile His His Leu Lys
1 5 10 15

Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp
20 25 30

Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
35 40 45

Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Pro
50 55 60

Ile Leu Ser Asn Leu Gln Pro Cys Val Pro Tyr Trp Thr Ala Pro Pro
65 70 75 80

Ser Arg Thr Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
85 90 95

Leu Lys Leu Gln Phe Tyr Leu Ser Thr Leu Glu Gln Ala Gln Glu Gln
100 105 110

Gln

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Leu Ile His His Leu Lys

1 5 10 15
 Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp
 20 25 30
 Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Ala
 50 55 60
 Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
 65 70 75 80
 Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Leu Lys Leu Gln Phe Tyr Leu Ser Ser Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Leu Ile His His Leu Lys
 1 5 10 15
 Ile Pro Pro Asn Pro Ser Leu Asp Ser Ala Asn Leu Asn Ser Glu Asp
 20 25 30
 Val Ser Ile Leu Met Glu Arg Asn Leu Arg Thr Pro Asn Leu Leu Ala
 35 40 45
 Phe Val Arg Ala Val Lys His Leu Glu Asn Ala Ser Gly Ile Glu Pro
 50 55 60
 Ile Leu Ser Asn Leu Gln Pro Cys Val Pro Tyr Trp Thr Ala Pro Pro
 65 70 75 80
 Ser Arg Thr Pro Ile Thr Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
 85 90 95
 Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
 100 105 110
 Gln

(2) INFORMATION FOR SEQ ID NO:331:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

Met Ala Asn Cys Ser Ile Met Ile Asp Glu Ala Ile His His Leu Lys
1           5           10           15

Arg Pro Pro Ala Pro Ser Leu Asp Pro Asn Asn Leu Asn Asp Glu Asp
          20           25           30

Met Ser Ile Leu Met Asp Arg Asn Leu Arg Leu Ser Asn Leu Glu Ser
          35           40           45

Phe Val Arg Ala Val Lys Asn Leu Glu Asn Ala Ser Gly Ile Glu Ala
          50           55           60

Ile Leu Arg Asn Leu Gln Pro Cys Leu Pro Ser Ala Thr Ala Ala Pro
65           70           75           80

Ser Arg His Pro Ile Ile Ile Lys Ala Gly Asp Trp Gln Glu Phe Arg
          85           90           95

Glu Lys Leu Thr Phe Tyr Leu Val Thr Leu Glu Gln Ala Gln Glu Gln
          100          105          110

Gln
  
```

(2) INFORMATION FOR SEQ ID NO:332:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

ATGGCAAAC TCTCTATAGC TATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC      60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC      120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA      180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC      240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATCCGGGA AAAACTGACG      300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG                                339
  
```


(2) INFORMATION FOR SEQ ID NO:333:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

ATGGCAA	ACT	GCTCTATAAT	CATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCC	GAAGACATGG	ATATCCTGAT	GGAACGAAAC		120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA		180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC		240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCGGGA	AAAAC	TGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG				339

(2) INFORMATION FOR SEQ ID NO:334:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

ATGGCTAACT	GCTCTATAAT	GATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60	
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGAT	GGAACGAAAC	120	
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180	
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240	
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCGGGA	AAAAC	TGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG				339

(2) INFORMATION FOR SEQ ID NO:335:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

Figure 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

ATGGCAAACT	GCTCTATAGC	TATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAAC TGACG	300
TTCTATCTGG	TTACCCCTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEO ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

ATGGCAAAC	TCTCTATAAT	GATCCATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGAT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCCGGGA	AAAACCTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEO ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT CGAACGAAAC 120

CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGCT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGGA CGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

ATGGCAAAC	GCTCTATAGC	TATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGAT	CGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCGGGA	AAAACGTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

ATGGCAAAC	GCTCTATAAT	CATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGAT	CGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCGGGA	AAAACGTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

ATGGCAAAC	GCTCTATAGC	TATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGCT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCGGGA	AAAACCTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

ATGGCAAAC	GCTCTATAAT	CATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGCT	GGAACGAAAC	120
CTTCGAACTC	CAAACCTGCT	CGCATTCGTA	AGGGCTGTCA	AGCACTTAGA	AAATGCATCA	180
GGTATTGAGG	CAATTCTTCG	TAATCTCCAA	CCATGTCTGC	CCTCTGCCAC	GGCCGCACCC	240
TCTCGACATC	CAATCATCAT	CAAGGCAGGT	GACTGGCAAG	AATTCGGGA	AAAACCTGACG	300
TTCTATCTGG	TTACCCTTGA	GCAAGCGCAG	GAACAACAG			339

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

ATGGCAAAC	GCTCTATAGC	TATCGATGAA	ATTATACATC	ACTTAAAGAG	ACCACCTAAC	60
CCTTTGCTGG	ACCCGAACAA	CCTCAATTCT	GAAGACGTTG	ATATCCTGGA	CGAACGAAAC	120

```
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA      180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC      240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG      300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG                               339
```

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```
ATGGCAAAC TCTCTATAAT CATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC      60
CCTTTGCTGG ACCCGAACAA CCTCAATTCT GAAGACGTTG ATATCCTGGA CGAACGAAAC      120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA      180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC      240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG      300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG                               339
```

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

```
ATGGCTAACT GCTCTATTAT GATCGATGAA GCAATACATC ACTTAAAGGT TCCACCTGCA      60
CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC      120
CTTCGACTTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA      180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC      240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG      300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG                               339
```

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGGT TCCACCTGCA	60
CCTTTGCTGG ACAGTAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTTT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATAAC GAAGACGTTT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTTT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTTT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACATGT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:353:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACATGT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:354:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAAGTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:355:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAAGTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA G	321

(2) INFORMATION FOR SEQ ID NO:356:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

ATGGATAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA 300
TTCTATCTGG TTACCCTTGA G 321

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATTCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA 300
TTCTATCTGG TTACCCTTGA G 321

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180

GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA G 321

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTTT CTATCCTGAT GGACCGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAAGTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGCAA 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGGT ACCACCTCGC 60
CCTTCCCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC 120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAAGTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCTGG CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTTT CTATTCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGCAA	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGCAA	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGACCGAAAC	120
CTTCGACTTA GCAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240

TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
 CCTTCCCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC C 120
 CTTGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
 CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCG ATATCCTGAT GGAACGAAAC 120
 CTTGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:370:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGGT ACCACCTCGC	60
CCTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCT ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CCGTATGGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCT ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCTGG CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240

TCTCGACATC CAATCATCAT CCGTATGGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
 CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC 120
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:374:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGGT ACCACCTCGC 60
 CCTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGAACGAAAC 120
 CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
 TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:375:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGCAA	300
TTCTATCTGG TTACCCTTGA G	321

(2) INFORMATION FOR SEQ ID NO:376:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
 CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCG ATTCTCTGAT GGAACGAAAC 120
 CTTGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
 TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA 60
 CCTTTGCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCG TGTCTCTGAT GGAACGAAAC 120
 CTTGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
 TTCTATCTGG TTACCCCTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGAC 60
 CTTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACGTCT CTATCCTGAT GGACCGAAAC 120
 CTTGACTTA GCAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA 180
 GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
 TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG

339

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTA GCAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

ATGGCTAACT GCTCTATAAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTCCCTGG ACCCGAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGACCGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGCAA	300
TTCTATCTGT GGACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

ATGGATAACT GCTCTATTAT GATCGATGAA GCAATACATC ACTTAAAGAG ACCACCTGCA	60
CCTTTGCTGG ACCCGAACAA CCTCAATGCT GAAGACGTCG ATATCCTGAT GGAACGAAAC	120
CTTCGACTTC CAAACCTGGA GAGCTTCGTA AGGGCTGTCA AGAACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

ATGGCTAACT GCTCTATAAT GCCAGATGAA GCAATACATC ACTTAAAGAT ACCACCTAAC	60
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CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:385:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:386:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

ATGGCTAACT GCTCTATTAT GATCGATGAA GCAATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300

TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG

339

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

ATGGCTAACT GCTCTATAAT ACTCGATGAA GCAATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGACTCCAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCCTA CATGCTGTCA AGCAATTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGACTCCAAC 120
CTTCGAACTC CAAACCTGCT CGCATTCCCA CATGCTTCTA AGCAATTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGGA AAAACTGACG 300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC 120
CTTCGAACTC CAAACCTGCT CGCATTCTGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA 180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC 240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATTCCGGCT TAAACTGCAA 300
TTCTATCTGT CTACCCTTGA GCAAGCGCAG GAACAACAG 339

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC 60

CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATCCGGCT TAAACTGCAA	300
TTCTATCTGT CTACCCTT	318

(2) INFORMATION FOR SEQ ID NO:392:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATCCGGCT TAAACTGCAA	300
TTCTATCTGT CTTCTCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:393:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGC CAATTCTTTC TAATCTCCAA CCATGTGTTC CCTATTGGAC GGCCCTCCC	240
TCTCGAACAC CAATCACGAT CAAGGCAGGT GACTGGCAAG AATCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAG ACCACCTAAC	60
CCTTTGCTGG ACCCGAACAA CCTCAATTCC GAAGACATGG ATATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGC CAATTCTTTC TAATCTCCAA CCATGTGTTC CCTATTGGAC GGCCCCTCCC	240
TCTCGAACAC CAATCACGAT CAAGGCAGGT GACTGGCAAG AATTCCGGCT TAAACTGCAA	300
TTCTATCTGT CTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGC CAATTCTTTC TAATCTCCAA CCATGTGTTC CCTATTGGAC GGCCCCTCCC	240
TCTCGAACAC CAATCACGAT CAAGGCAGGT GACTGGCAAG AATTCCGGCT TAAACTGCAA	300
TTCTATCTGT CTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGG CAATTCTTCG TAATCTCCAA CCATGTCTGC CCTCTGCCAC GGCCGCACCC	240
TCTCGACATC CAATCATCAT CAAGGCAGGT GACTGGCAAG AATCCGGCT TAAACTGCAA	300
TTCTATCTGT CTTCTCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

ATGGCTAACT GCTCTATAAT GATCGATGAA ATTATACATC ACTTAAAGAT ACCACCTAAC	60
CCTAGCCTGG ACAGTGCTAA CCTCAATTCC GAAGACGTCT CTATCCTGAT GGAACGAAAC	120
CTTCGAACTC CAAACCTGCT CGCATTCGTA AGGGCTGTCA AGCACTTAGA AAATGCATCA	180
GGTATTGAGC CAATTCTTTC TAATCTCCAA CCATGTGTTC CCTATTGGAC GGCCCCCTCC	240
TCTCGAACAC CAATCACGAT CAAGGCAGGT GACTGGCAAG AATCCGGGA AAAACTGACG	300
TTCTATCTGG TTACCCTTGA GCAAGCGCAG GAACAACAG	339

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGACAATAAC	120

CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA 180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC 240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC 300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAG 339

(2) INFORMATION FOR SEQ ID NO:399:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG 60
CCGCTGCTGG ACTTCAACAA CCTCAATGAC GAAGACATGT CTATCCTGAT GGAAAATAAC 120
CTTCGTCGTC CAAACCTCGA GGCATTCAAC CGTGCTGTCA AGTCTCTGCA GAATGCATCA 180
GCAATTGAGA GCATTCTTAA AAATCTCCTG CCATGTCTGC CCCTGGCCAC GGCCGCACCC 240
ACGCGACATC CAATCCATAT CAAGGACGGT GACTGGAATG AATTCCGTCG TAAACTGACC 300
TTCTATCTGA AAACCTTGGA GAACGCGCAG GCTCAACAG 339

(2) INFORMATION FOR SEQ ID NO:400:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

AAGGAGATAT ATCCATGAAC TGCTCTAAC 29

(2) INFORMATION FOR SEQ ID NO:401:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Met Asn Cys Ser Asn
1 5

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln
1 5 10 15
Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln
20 25 30
Asp Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe
35 40 45
Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile
50 55 60
Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr
65 70 75 80
Arg His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg
85 90 95
Lys Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110
Thr Thr Leu Arg Leu Ala Ile Phe
115 120

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Met Ala Tyr Pro Glu Thr Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:404:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

ATGGCATATC CAGAACTGA TTACAAGGAC GACGATGACA AGGCTAACTG CTCTATAATG	60
ATCGATGAAA TTATACATCA CTTAAAGAGA CCACCTGCAC CTTTGCTGGA CCCGAACAAC	120
CTCAATGCTG AAGACGTCGA TATCCTGATG GAACGAAACC TTCGACTTCC AAACCTGGAG	180
AGCTTCGTAA GGGCTGTCAA GAACTTAGAA AATGCATCAG GTATTGAGGC AATTCTTCGT	240
AATCTCCAAC CATGTCTGCC CTCTGCCACG GCCGCACCCT CTCGACATCC AATCATCATC	300
AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA AACTGACGT TCTATCTGGT TACCCTTGAG	360
CAAGCGCAGG AACAACAG	378

(2) INFORMATION FOR SEQ ID NO:405:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

ATGGCATATC CAGAACTGA TTACAAGGAC GACGATGACA AGGCTAACTG CTCTATAATG	60
ATCGATGAAA TTATACATCA CTTAAAGAGA CCACCTAACC CTTTGCTGGA CCCGAACAAC	120
CTCAATTCCG AAGACATGGA TATCCTGATG GAACGAAACC TTCGAACTCC AAACCTGCTC	180
GCATTCGTAA GGGCTGTCAA GCACTTAGAA AATGCATCAG GTATTGAGGC AATTCTTCGT	240
AATCTCCAAC CATGTCTGCC CTCTGCCACG GCCGCACCCT CTCGACATCC AATCATCATC	300
AAGGCAGGTG ACTGGCAAGA ATTCCGGGAA AACTGACGT TCTATCTGGT TACCCTTGAG	360
CAAGCGCAGG AACAACAG	378

(2) INFORMATION FOR SEQ ID NO:406:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Ala Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys
1 5 10 15
Gln Pro Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Asp Glu Asp
20 25 30
Met Ser Ile Leu Met Glu Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala
35 40 45
Phe Asn Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser
50 55 60
Ile Leu Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro
65 70 75 80
Thr Arg His Pro Ile Ile Ile Arg Asp Gly Asp Trp Asn Glu Phe Arg
85 90 95
Arg Lys Leu Thr Phe Tyr Leu Trp Thr Leu Glu Asn Ala Gln Ala Gln
100 105 110
Gln

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Asn Cys Ser Asn Met Ile Asp Glu Ile Ile Thr His Leu Lys Gln Pro
1 5 10 15
Pro Leu Pro Leu Leu Asp Phe Asn Asn Leu Asn Gly Glu Asp Gln Asp
20 25 30
Ile Leu Met Asp Asn Asn Leu Arg Arg Pro Asn Leu Glu Ala Phe Asn
35 40 45
Arg Ala Val Lys Ser Leu Gln Asn Ala Ser Ala Ile Glu Ser Ile Leu
50 55 60
Lys Asn Leu Leu Pro Cys Leu Pro Leu Ala Thr Ala Ala Pro Thr Arg
65 70 75 80
His Pro Ile His Ile Lys Asp Gly Asp Trp Asn Glu Phe Arg Arg Lys
85 90 95

Leu Thr Phe Tyr Leu Lys Thr Leu Glu Asn Ala Gln Ala Gln Gln
100 105 110

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

ATGGCTAACT GCTCTAACAT GATCGATGAA ATCATCACCC ACCTGAAGCA GCCACCGCTG	60
CCGCTGCTGG ACTTCAACAA CCTCAATGGT GAAGACCAAG ATATCCTGAT GGAACAATAA	120
CCTTCGTCGT CCAAACCTCG AGGCATTCAA CCGTGCTGTC AACTCTCTGC AGAATGCATC	180
AGCAATTGAG AGCATTCTTA AAAATCTCCT GCCATGTCTG CCCCTGGCCA CGGCCGCACC	240
CACGCGACAT CCAATCCATA TCAAGGACGG TGACTGGAAT GAATTCCGTC GTAAACTGAC	300
CTTCTATCTG AAAACCTTGG AGAACGCGCA GGCTCAACAG	340

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

CTTTAAGTGA TGTATAATTT CATCGATCAT TATAGAGCAG TTAGC	45
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(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CACTTAAAGA GACCACCTGC ACCTTTGCTG GACCCG	36
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(2) INFORMATION FOR SEQ ID NO:411:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GAGGTTGTTT GGGTCCAGCA AAGGTGCAGG TGGTCT

36

(2) INFORMATION FOR SEQ ID NO:412:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

CACTTAAAGA GACCACCTAA CCCTTTGCTG GACCCG

36

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GAGGTTGTTT GGGTCCAGCA AAGGGTTAGG TGGTCT

36

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

CACTTAAAGG TTCCACCTGC ACCTTTGCTG GACAGT

36

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GAGGTTGTTA CTGTCCAGCA AAGGTGCAGG TGGAAC

36

CACTTAAAGG TTCCACCTGC ACCTTTGCTG GACAGT